

GenCore version 4.5
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OM protein - protein search, using sw model
Run on: January 9, 2002, 15:01:13 ; Search time 83.2 Seconds
(without alignments)
16.025 Million cell updates/sec

Title: US-09-828-000-6
Perfect score: 96
Sequence: 1 VIFNYKKNVLINKDIRC 18
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5
Searched: 522463 seqs, 74073290 residues
Total number of hits satisfying chosen parameters: 522463
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_1101.*
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21: /SIDS8/gcgdata/geneseq/geneseq/AA2000.DAT.*
22: /SIDS8/gcgdata/geneseq/geneseq/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	96	100.0	60	21	AA192354 Recombinant human
2	96	100.0	61	21	AA192352 Recombinant human
3	96	100.0	180	21	AA192351 Human vasostatin (
4	96	100.0	280	21	AA192355 Recombinant delta-
5	96	100.0	400	21	AA192350 Recombinant human
6	96	100.0	401	18	AA111156 Calreticulin. Hom
7	96	100.0	417	10	AA192276 60 kD Ro (Ro/SSA)
8	96	100.0	417	20	AA190927 Calreticulin. Hom
9	96	100.0	417	21	AA192349 Human MBP-calretic
10	91	94.8	403	17	AA192347 Flea calreticulin
11	82	85.4	49	21	AA192353 Recombinant human

12	66	68.8	336	12	AA123112	Partial sequence o
13	51	53.1	848	21	AA188565	Human NCAM 140kd 1
14	48	50.0	17	20	AA121879	Peptide Seq ID No:
15	48	50.0	17	20	AA109101	Cell adhesion reco
16	48	50.0	17	21	AA178215	N-CAM heparin bind
17	48	50.0	17	21	AA164629	Cell adhesion reco
18	44	45.8	295	22	AA164666	S. pombe Chk1 kina
19	44	45.8	496	22	AA100857	Schizosaccharomyce
20	43	44.8	14	21	AA110751	Fibrin gel binding
21	43	44.8	14	21	AA101586	Proteoglycan bindi
22	43	44.8	14	22	AA135931	NCAM/heparin bindi
23	43	44.8	22	21	AA110761	Fibrin gel binding
24	43	44.8	318	20	AA128509	Fen(Y205D) mutant
25	43	44.8	415	22	AA166341	Castor bean calret
26	43	44.8	415	22	AA166343	Castor bean calret
27	43	44.8	805	21	AA128141	Sucrose synthase p
28	43	44.8	805	21	AA116282	Eucalyptus grandis
29	43	44.8	805	21	AA116336	Eucalyptus grandis
30	41	42.7	122	10	AA190402	Plasmodium falcipa
31	41	42.7	198	21	AA158162	Lung cancer associ
32	41	42.7	236	22	AA125835	Human protein sequ
33	41	42.7	238	21	AA121100	Human brain ring-f
34	41	42.7	250	18	AA125144	Memordin (a riboso
35	41	42.7	250	18	AA121707	Memordin. Momordi
36	41	42.7	255	22	AA173609	Human colon cancer
37	41	42.7	263	14	AA137296	Plant type I RIP M
38	41	42.7	263	16	AA163908	Type I ribosome-in
39	41	42.7	263	16	AA174182	Type I ribosome-in
40	41	42.7	355	22	AA175504	Human colon cancer
41	41	42.7	502	12	AA115226	HincII restriction
42	41	42.7	503	15	AA155366	Human Activin rece
43	41	42.7	503	16	AA185210	Human ALK-1. Homo
44	41	42.7	503	17	AA194602	TAR-3 polypeptide.
45	41	42.7	503	18	AA127507	Human activin rece

ALIGNMENTS

RESULT 1
AA192354
ID AA192354 standard; Protein; 60 AA.
XX
AC AA192354;
XX
DT 10-AUG-2000 (first entry)
XX
DE Recombinant human calreticulin residues 121-180.

XX MBP-calreticulin; maltose binding protein; angiogenesis; inhibition;
KW endothelial cell; anti-angiogenic; neuroprotective; antidiabetic;
KW cytostatic; dermalogical; immunosuppressive; antiinflammatory; hepatic;
KW anti-atherosclerotic; gastrointestinal; anti-arthritic; ophthalmic.

OS Homo sapiens.
OS Synthetic.
XX
PN WO200020577-A1.

XX
PD 13-APR-2000.
XX
PF 05-OCT-1999; 99WO-US23240.
XX
PR 06-OCT-1998; 98US-0103438.

XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Tosato G, Pike SE, Yao L;
XX WPI; 2000-303767/26.
DR
XX Inhibiting endothelial cell growth and angiogenesis using calreticulin,
PT useful for suppressing tumor growth

XX PS Claim 4; Page 85; 99pp; English.

XX CC A novel method of inhibiting endothelial cell growth comprises

CC contacting the cells with calreticulin (or its fragments/variants).

CC Fragments of calreticulin causes at least 40% inhibition of angiogenesis,

CC tumor growth and/or endothelial cell growth (claimed). The method may be

CC used for inhibiting angiogenesis in a patient. The angiogenesis is

CC associated with a disease other than a tumor that is associated with

CC neovascularization (e.g. diabetic neuropathy, retrolental fibroplasia,

CC trachoma, neovascular glaucoma, psoriasis, angiofibromas, immune

CC inflammation, atherosclerosis, excessive wound repair, retinal

CC neovascularization, macular degeneration, corneal graft rejection,

CC contact lens overwear, Crohn's disease, non-immune inflammation,

CC rheumatoid arthritis, systemic lupus erythematosus, thyroiditis,

CC Goodpasture's syndrome, systemic vasculitis, scleroderma, Sjorgen's

CC syndrome, sarcoidosis and primary biliary cirrhosis). The method may

CC also be used for treating/inhibiting tumor growth especially

XX Kaposi's sarcoma (claimed).

SQ Sequence 60 AA;

Query Match 100.0%; Score 96; DB 21; Length 60;

Best Local Similarity 100.0%; Pred. No. 1.7e-09;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VIFNYGKNVINKDIRC 18

XXXXXXXXXXXXXXXXXX

DB 9 VIFNYGKNVINKDIRC 26

RESULT 2

AAY92352

ID AAY92352 standard; Protein; 61 AA.

XX AC AAY92352;

XX 10-AUG-2000 (first entry)

XX Recombinant human calreticulin residues 120-180.

XX MBP-calreticulin; maltose binding protein; angiogenesis; inhibition;

KW endothelial cell; anti-angiogenic; neuroprotective; antidiabetic;

KW cytotatic; dermalogical; immunosuppressive; antiinflammatory; hepatic;

KW anti-atherosclerotic; gastrointestinal; anti-arthritis; ophthalmic.

XX OS Homo sapiens.

XX OS Synthetic.

XX WO200020577-A1.

XX 13-APR-2000.

XX 05-OCT-1999; 99WO-US23240.

XX 06-OCT-1998; 98US-0103438.

XX (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX Tosato G, Pike SE, Yao L;

XX WPI; 2000-303767/26.

XX Inhibiting endothelial cell growth and angiogenesis using calreticulin,

PT useful for suppressing tumor growth

XX Claim 4; Page 82-83; 99pp; English.

XX A novel method of inhibiting endothelial cell growth comprises

CC contacting the cells with calreticulin (or its fragments/variants).

CC Fragments of calreticulin causes at least 40% inhibition of angiogenesis,

CC tumor growth and/or endothelial cell growth (claimed). The method may be

CC used for inhibiting angiogenesis in a patient. The angiogenesis is

CC associated with a disease other than a tumor that is associated with

CC neovascularization (e.g. diabetic neuropathy, retrolental fibroplasia,

CC trachoma, neovascular glaucoma, psoriasis, angiofibromas, immune

CC inflammation, atherosclerosis, excessive wound repair, retinal

CC neovascularization, macular degeneration, corneal graft rejection,

CC contact lens overwear, Crohn's disease, non-immune inflammation,

CC rheumatoid arthritis, systemic lupus erythematosus, thyroiditis,

CC Goodpasture's syndrome, systemic vasculitis, scleroderma, Sjorgen's

CC syndrome, sarcoidosis and primary biliary cirrhosis). The method may

CC also be used for treating/inhibiting tumor growth especially

XX Kaposi's sarcoma (claimed).

SQ Sequence 61 AA;

Query Match 100.0%; Score 96; DB 21; Length 61;

Best Local Similarity 100.0%; Pred. No. 1.7e-09;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VIFNYGKNVINKDIRC 18

XXXXXXXXXXXXXXXXXX

DB 10 VIFNYGKNVINKDIRC 27

RESULT 3

AAY92351

ID AAY92351 standard; Protein; 180 AA.

XX AC AAY92351;

XX 10-AUG-2000 (first entry)

XX Human vasostatin (calreticulin N-terminal 180 amino acids).

XX MBP-calreticulin; maltose binding protein; vasostatin; N-terminal;

KW angiogenesis; inhibition; endothelial cell; anti-angiogenic;

KW neuroprotective; antidiabetic; cytotatic; dermalogical; hepatic;

KW immunosuppressive; antiinflammatory; anti-atherosclerotic;

KW gastrointestinal; anti-arthritis; ophthalmic.

XX OS Homo sapiens.

XX OS Synthetic.

XX WO200020577-A1.

XX 13-APR-2000.

XX 05-OCT-1999; 99WO-US23240.

XX 06-OCT-1998; 98US-0103438.

XX (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX Tosato G, Pike SE, Yao L;

XX WPI; 2000-303767/26.

XX Inhibiting endothelial cell growth and angiogenesis using calreticulin,

PT useful for suppressing tumor growth

XX Claim 4; Page 82; 99pp; English.

XX A novel method of inhibiting endothelial cell growth comprises

CC contacting the cells with calreticulin (or its fragments/variants).

CC Fragments of calreticulin causes at least 40% inhibition of angiogenesis,

CC tumor growth and/or endothelial cell growth (claimed). The method may be

CC used for inhibiting angiogenesis in a patient. The angiogenesis is

CC associated with a disease other than a tumor that is associated with

CC neovascularization (e.g. diabetic neuropathy, retrolental fibroplasia,

CC trachoma, neovascular glaucoma, psoriasis, angiofibromas, immune

CC inflammation, atherosclerosis, excessive wound repair, retinal

CC neovascularization, macular degeneration, corneal graft rejection,

CC contact lens overwear, Crohn's disease, non-immune inflammation,
 CC Rheumatoid arthritis, systemic lupus erythematosus, thyroiditis,
 CC Goodpasture's syndrome, systemic vasculitis, scleroderma, Sjorgen's
 CC syndrome, sarcoidosis and primary biliary cirrhosis). The method may
 CC also be used for treating/inhibiting tumor growth especially
 CC Kaposi's sarcoma (claimed).
 XX
 SQ Sequence 180 AA;

Query Match 100.0%; Score 96; DB 21; Length 180;
 Best Local Similarity 100.0%; Pred. No. 6.4e-09;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VIFNYGKNVLINKDIRC 18
 Db 129 vifnygknvlinkdirc 146
 |||||

RESULT 4
 AAY92355
 ID AAY92355 standard; Protein: 280 AA.
 XX
 AC AAY92355;
 XX
 DT 10-AUG-2000 (first entry)
 XX
 DE Recombinant delta-120 calreticulin.
 XX
 KW MBP-calreticulin; maltose binding protein; angiogenesis; inhibition;
 KW endothelial cell; anti-angiogenic; neuroprotective; antidiabetic;
 KW cytostatic; dermatological; immunosuppressive; antiinflammatory; hepatic;
 KW anti-atherosclerotic; gastrointestinal; anti-arthritis; ophthalmic.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 PN WO200020577-A1.
 XX
 PD 13-APR-2000.
 XX
 PF 05-OCT-1999; 99WO-US23240.
 XX
 PR 06-OCT-1998; 98US-0103438.
 XX
 PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
 XX
 PI Tosato G, Pike SE, Yao L;
 XX
 PS WPI; 2000-303767/26.
 XX
 PT Inhibiting endothelial cell growth and angiogenesis using calreticulin,
 PT useful for suppressing tumor growth
 XX
 PS Claim 4; Page 86; 99pp; English.
 XX
 CC This sequence comprises recombinant human calreticulin (AAY92350)
 CC missing the N-terminal 120 amino acids.
 CC A novel method of inhibiting endothelial cell growth comprises
 CC contacting the cells with calreticulin (or its fragments/variants).
 CC Fragments of calreticulin causes at least 40% inhibition of
 CC angiogenesis, tumor growth and/or endothelial cell growth (claimed). The
 CC method may be used for inhibiting angiogenesis in a patient. The
 CC angiogenesis is associated with a disease other than a tumor that is
 CC associated with neovascularization (e.g. diabetic neuropathy, retrolental
 CC fibroplasia, trachoma, neovascular glaucoma, psoriasis, angiofibromas,
 CC immune inflammation, atherosclerosis, excessive wound repair, retinal
 CC neovascularization, macular degeneration, corneal graft rejection,
 CC contact lens overwear, Crohn's disease, non-immune inflammation,
 CC rheumatoid arthritis, systemic lupus erythematosus, thyroiditis,
 CC Goodpasture's syndrome, systemic vasculitis, scleroderma, Sjorgen's
 CC syndrome, sarcoidosis and primary biliary cirrhosis). The method may
 CC also be used for treating/inhibiting tumor growth especially

CC Kaposi's sarcoma (claimed).
 XX
 SQ Sequence 280 AA;

Query Match 100.0%; Score 96; DB 21; Length 280;
 Best Local Similarity 100.0%; Pred. No. 1.1e-08;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VIFNYGKNVLINKDIRC 18
 Db 9 vifnygknvlinkdirc 26
 |||||

RESULT 5
 AAY92350
 ID AAY92350 standard; Protein: 400 AA.
 XX
 AC AAY92350;
 XX
 DT 10-AUG-2000 (first entry)
 XX
 DE Recombinant human MBP-calreticulin.
 XX
 KW MBP-calreticulin; maltose binding protein; angiogenesis; inhibition;
 KW endothelial cell; anti-angiogenic; neuroprotective; antidiabetic;
 KW cytostatic; dermatological; immunosuppressive; antiinflammatory; hepatic;
 KW anti-atherosclerotic; gastrointestinal; anti-arthritis; ophthalmic.
 XX
 OS Homo sapiens.
 PN WO200020577-A1.
 XX
 PD 13-APR-2000.
 XX
 PF 05-OCT-1999; 99WO-US23240.
 XX
 PR 06-OCT-1998; 98US-0103438.
 XX
 PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
 XX
 PI Tosato G, Pike SE, Yao L;
 XX
 DR WPI; 2000-303767/26.
 DR N-PSDB; AAA09346, AAA09347.
 XX
 PT Inhibiting endothelial cell growth and angiogenesis using calreticulin,
 PT useful for suppressing tumor growth
 XX
 PS Claim 4; Page 80-81; 99pp; English.
 XX
 CC Recombinant human MBP-calreticulin comprises the sequence of human
 CC calreticulin (see AAY92349) without the 17 N-terminal amino acids.
 CC A novel method of inhibiting endothelial cell growth comprises
 CC contacting the cells with calreticulin (or its fragments/variants).
 CC Fragments of calreticulin causes at least 40% inhibition of
 CC angiogenesis, tumor growth and/or endothelial cell growth (claimed). The
 CC method may be used for inhibiting angiogenesis in a patient. The
 CC angiogenesis is associated with a disease other than a tumor that is
 CC associated with neovascularization (e.g. diabetic neuropathy, retrolental
 CC fibroplasia, trachoma, neovascular glaucoma, psoriasis, angiofibromas,
 CC immune inflammation, atherosclerosis, excessive wound repair, retinal
 CC neovascularization, macular degeneration, corneal graft rejection,
 CC contact lens overwear, Crohn's disease, non-immune inflammation,
 CC rheumatoid arthritis, systemic lupus erythematosus, thyroiditis,
 CC Goodpasture's syndrome, systemic vasculitis, scleroderma, Sjorgen's
 CC syndrome, sarcoidosis and primary biliary cirrhosis). The method may
 CC also be used for treating/inhibiting tumor growth especially
 CC Kaposi's sarcoma (claimed).
 XX
 SQ Sequence 400 AA;

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Query Match      100.0%; Score 96; DB 21; Length 400;
Best Local Similarity 100.0%; Pred. No. 1.7e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VIFNYGKNVINKDIRC 18
DB 129 VIFNYGKNVINKDIRC 146

RESULT 6
AAW11156
ID AAW11156 standard; peptide; 401 AA.
XX
AC AAW11156;
XX
DT 31-MAY-1997 (first entry)
XX
DE Calreticulin.
XX
KW calreticulin; C-domain; restenosis; inhibitor.
XX
OS Homo sapiens.
XX
PN WO9636643-A1.
XX
PD 21-NOV-1996.
XX
PF 17-MAY-1996; 96WO-1B00471.
XX
PR 16-MAY-1996; 96US-0649417.
XX
PS 17-MAY-1995; 95US-0442844.
XX
PA (UYAL-) UNIV ALBERTA.
XX
PI LUCAS A, Michalak M;
XX
WPI; 1997-012036/01.
XX
Inhibition of restenosis in patients - using calreticulin or a
C-domain polypeptide of calreticulin or a variant with the same
activity.
XX
Dislosure; Fig 1; 48pp; English.
XX
The present sequence is calreticulin. It and a C-domain derived peptide
(AAW06736) are useful for treating a patient to inhibit restenosis. The
calreticulin-type cpds. are administered either parenterally,
intravenously or via a catheter and can target areas of vascular damage
to inhibit or prevent restenosis.
XX
Sequence 401 AA;

Query Match      100.0%; Score 96; DB 18; Length 401;
Best Local Similarity 100.0%; Pred. No. 1.7e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VIFNYGKNVINKDIRC 18
DB 129 VIFNYGKNVINKDIRC 146

RESULT 7
AAP92276
ID AAP92276 standard; protein; 417 AA.
XX
AC AAP92276;
XX
DT 23-FEB-1990 (first entry)
XX
DK 60 kD Ro (Ro/SSA) antigen.
XX
SJORIN syndrome; systemic lupus erythematosus.
XX

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XX Synthetic.
OS WO8909273-A.
PN
XX
XX 05-OCT-1989.
XX
XX 22-MAR-1989; 89WO-US01213.
XX
XX 22-MAR-1988; 88US-0171634.
XX
XX (TEXA ) UNIV OF TEXAS SYST.
XX
XX Sontheimer RD, Capra JD, McCauliffe DP;
XX
XX WPI; 1989-309537/42.
XX
XX N-PSDB; AAP92276.
XX
DNA sequences encoding antigenic epitope(s) of Ro 60 kD autoantigen
- used in immunoassays to detect rheumatic disease
XX
Dislosure; Fig 2; 88pp; English.
XX
Synthetic peptides corresp. to an epitopic core of Ro antigen are
expressed recombinantly to detect autoantibodies, for identification
of autoimmune diseases. These epitopes are AAs 24-36, 23-36, 188-209,
or 241-255. The peptides may be substd. for ribonucleoprotein particle
antigens.
XX
Sequence 417 AA;

Query Match      100.0%; Score 96; DB 10; Length 417;
Best Local Similarity 100.0%; Pred. No. 1.8e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VIFNYGKNVINKDIRC 18
DB 146 VIFNYGKNVINKDIRC 163

RESULT 8
AAY00927
ID AAY00927 standard; Protein; 417 AA.
XX
AC AAY00927;
XX
DT 28-MAY-1999 (first entry)
XX
DE Calreticulin.
XX
KW Clq and collectin receptor; cC1qR binding domain; complement ubiquitin;
KW CUB functionality; inhibitor; complement activation; inflammation;
KW myocardial infarction; brain ischaemia; gut ischaemia; amyloid plaque;
KW rheumatoid arthritis; systemic lupus erythematosus; Alzheimer's disease;
KW immune complex nephritis; therapy.
XX
OS Homo sapiens.
XX
PN WO9507406-A1.
XX
PD 18-FEB-1999.
XX
PF 12-AUG-1998; 98WO-GB02430.
XX
PR 12-AUG-1997; 97GB-0016998.
XX
PA (UYLE-) UNIV LEICESTER.
XX
PI Schwaeble W;
XX
XX WPI; 1999-180404/15.
XX

```


PT Use of a cClqR binding domain - to modulate complement ubiquitin
 PT (CUB) functionality.

XX
 XX
 PS Disclosure: Page 26-27; 31pp; English.

XX This sequence is calreticulin, a homologue of Clq and collectin receptor
 CC (cClqR). The invention relates to the use of a cClqR binding domain in a
 CC medicament to effect complement ubiquitin (CUB) functionality, and an
 CC inhibitor of the cClqR binding domain in a medicament to inhibit CUB
 CC functionality. The cClqR binding domain, or its inhibitor, can be used to
 CC treat a human or animal body. Particularly an inhibitor is used to treat
 CC complement activation involved in the initiation and maintenance of
 CC inflammation, for example in myocardial infarction, brain ischaemia
 CC (stroke), gut ischaemia, rheumatoid arthritis, systemic lupus
 CC erythematosus, burns, immune complex nephritis, and to treat amyloid
 CC plaques in Alzheimer's disease. The use of cClqR binding domain or
 CC inhibitor enables the CUB domain functionality to be modulated using a
 CC low molecular weight molecule.

XX Sequence 417 AA;

Query Match 100.0%; Score 96; DB 20; Length 417;
 Best Local Similarity 100.0%; Pred. No. 1.8e-08;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VIFNYKGNVLINKDIRC 18
 |||||
 Db 146 vifnykgnvlinkdirc 163

RESULT 9

AAW04171
 ID AAW04171 standard; Protein: 417 AA.

XX
 AC AAY92349;

XX 10-AUG-2000 (first entry)

XX Human MBP-calreticulin.

XX MBP-calreticulin; maltose binding protein; angiogenesis; inhibition;
 KW endothelial cell; anti-angiogenic; neuroprotective; antidiabetic;
 KW cytosolic; dermatological; immunosuppressive; antiinflammatory; hepatic;
 KW anti-atherosclerotic; gastrointestinal; anti-arthritis; ophthalmic.

XX Homo sapiens.

XX Key Location/Qualifiers
 FH Peptide 1..17
 FT /label= signal_peptide
 FT 18
 FT /label= mature_protein

XX WO200020577-A1.

XX 13-APR-2000.

XX 05-OCT-1999; 99WO-US23240.

XX 06-OCT-1998; 98US-0103438.

XX (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX Tosato G, Pike SE, Yao L;

XX WPI; 2000-303767/26.

XX N-PSDB; AAA09346, AAA09347.

XX Inhibiting endothelial cell growth and angiogenesis using calreticulin,
 PT useful for suppressing tumor growth

XX Disclosure: Page 79-80; 99pp; English.

XX A novel method of inhibiting endothelial cell growth comprises
 CC contacting the cells with calreticulin (or its fragments/variants).
 CC Fragments of calreticulin causes at least 40% inhibition of angiogenesis.
 CC tumor growth and/or endothelial cell growth (claimed). The method may be
 CC used for inhibiting angiogenesis in a patient. The angiogenesis is
 CC associated with a disease other than a tumor that is associated with
 CC neovascularization (e.g. diabetic neuropathy, retrolental fibroplasia,
 CC trachoma, neovascular glaucoma, psoriasis, angiofibromas, immune
 CC inflammation, atherosclerosis, excessive wound repair, retinal
 CC neovascularization, macular degeneration, corneal graft rejection,
 CC contact lens overwear, Crohn's disease, non-immune inflammation,
 CC rheumatoid arthritis, systemic lupus erythematosus, thyroiditis,
 CC Gyndpasture's syndrome, systemic vasculitis, scleroderma, Sjorgen's
 CC syndrome, sarcoidosis and primary biliary cirrhosis). The method may
 CC also be used for treating/inhibiting tumor growth especially
 CC Kaposi's sarcoma (claimed).

XX Sequence 417 AA;

Query Match 100.0%; Score 96; DB 21; Length 417;
 Best Local Similarity 100.0%; Pred. No. 1.8e-08;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VIFNYKGNVLINKDIRC 18
 |||||
 Db 146 vifnykgnvlinkdirc 163

RESULT 10

AAW04171
 ID AAW04171 standard; Protein: 403 AA.

XX
 AC AAW04171;

XX 12-DEC-1996 (first entry)

XX Flea calreticulin PctCal403.

XX Calreticulin; flea; haematophagous insect; allergic dermatitis;
 KW vaccine; therapy; PctCal403.

XX Ctenocephalides felis.

XX WO9628469-A1.

XX 19-SEP-1996.

XX 08-MAR-1996; 96WO-US03133.

XX 09-MAR-1995; 95US-0401509.

XX (HESK-) HESKA CORP.

XX Rushlow KE, Stiegler GL;

XX WPI; 1996-442861/44.

XX N-PSDB; AAT39516;

XX N-PSDB; AAT39517.

XX Haematophagous insect calreticulin protein - used to reduce insect
 PT infestation and desensitise patients to allergic dermatitis

XX Claim 5; Page 68-69; 86pp; English.

XX Flea calreticulin protein PctCall589 (AAW04171) is a calcium-binding
 CC protein found in the salivary glands of Ctenocephalides felis.

XX Its amino acid sequence was deduced from a cDNA clone (AAT39516)

CC obtd. from a salivary gland cDNA library. Recombinant PctCall589
 CC can be produced in host cells transformed with a vector carrying
 CC calreticulin nucleic acids. Calreticulin alters the blood feeding
 CC behaviour of haematophagous insects and can be administered to an

CC animal to reduce infestation. It reduces calreticulin activity in
 CC insects, so reducing the insect burden on an animal. Calreticulin
 CC can be used to elicit an immune response, thereby desensitising an
 CC animal to allergic dermatitis caused by fleas, mosquitoes or
 CC Culicoides.

XX SQ Sequence 403 AA;

Query Match 94.8%; Score 91; DB 17; Length 403;

Best Local Similarity 94.4%; Pred. No. 1.2e-07;

Matches 17; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 VIFNYKGNVLINKDIRC 18

DB 146 VIFS YKGNVLINKDIRC 163

RESULT 11

AA92353

ID AAY92353 standard; Protein; 49 AA.

XX AC AAY92353;

XX DT 10-AUG-2000 (first entry)

XX DE Recombinant human calreticulin residues 132-180.

XX KW MRP-calreticulin; maltose binding protein; angiogenesis; inhibition;
 KW endothelial cell; anti-angiogenic; neuroprotective; antidiabetic;
 KW cytostatic; dermatological; immunosuppressive; antiinflammatory; hepatic;
 KW anti-atherosclerotic; gastrointestinal; anti-arthritis; ophthalmic.

XX OS Homo sapiens.

XX SN Synthetic.

XX PN WO200020577-A1.

XX PD 13-APR-2000.

XX PF 05-OCT-1999; 99WO-US23240.

XX PR 06-OCT-1998; 98US-0103438.

XX PA (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX PI Tomato G, Pike SE, Yuo L;

XX WPI; 2000-303767/26.

XX PT Inhibiting endothelial cell growth and angiogenesis using calreticulin,
 PT useful for suppressing tumor growth

XX PS Claim 4; Page 82-83; 99pp; English.

XX CC A novel method of inhibiting endothelial cell growth comprises
 CC contacting the cells with calreticulin (or its fragments/variants).
 CC Fragments of calreticulin causes at least 40% inhibition of angiogenesis,
 CC tumor growth and/or endothelial cell growth (claimed). The method may be
 CC used for inhibiting angiogenesis in a patient. The angiogenesis is
 CC associated with a disease other than a tumor that is associated with
 CC neovascularization (e.g. diabetic neuropathy, retrolental fibroplasia,
 CC trachoma, neovascular glaucoma, psoriasis, angiofibromas, immune
 CC inflammation, atherosclerosis, excessive wound repair, retinal
 CC neovascularization, macular degeneration, corneal graft rejection,
 CC contact lens overwear, Crohn's disease, non-immune inflammation,
 CC rheumatoid arthritis, systemic lupus erythematosus, thyroiditis,
 CC Goodpasture's syndrome, systemic vasculitis, scleroderma, Sjorgen's
 CC syndrome, sarcoidosis and primary biliary cirrhosis). The method may
 CC also be used for treating/inhibiting tumor growth especially
 CC Kaposi's sarcoma (claimed).

XX SQ Sequence 49 AA;

Query Match 85.4%; Score 82; DB 21; Length 49;

Best Local Similarity 100.0%; Pred. No. 3.7e-07;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 NYKGNVLINKDIRC 18

DB 1 NYKGNVLINKDIRC 15

RESULT 12

AA912312

ID AAR12312 standard; Protein; 336 AA.

XX AC AAR12312;

XX DT 29-AUG-1991 (first entry)

XX DE Partial sequence of Onchocera volvulus 42 kD antigen.

XX KW River blindness; onchocerciasis; vaccine; antigen; parasite.

XX OS Onchocerca volvulus.

XX FH Key Location/Qualifiers

XX FT Region 160..166

XX FT /label= repeat unit

XX FT /note= "hydrophilic"

XX FT Region 177..183

XX FT /label= repeat unit

XX FT /note= "hydrophilic"

XX FT Region 195..201

XX FT /label= repeat unit

XX FT /note= "hydrophilic"

XX PN US5021342-A.

XX PD 04-JUN-1991.

XX PF 30-JUN-1988; 88US-0214264.

XX PR 30-JUN-1988; 88US-0214264.

XX PA (UYHO-) UNIV HOSPITALS CLEV.

XX PI Greene BM, Unnasch TR;

XX WPI; 1991-185179/25.

XX DR N-PSDB; AAQ11987.

XX PT DNA encoding Onchocerca volvulus antigen - used to express
 PT recombinant antigen for vaccine against onchocerciasis or river
 PT blindness.

XX PS Disclosure; Fig 7; 20pp; English.

XX CC The sequence was deduced from a cDNA clone lambda RAL-1 prepd.
 CC from RNA isolated from nodules excised from patients infected
 CC with O. volvulus. The N-terminal is incomplete, however Abs
 CC which specifically bind to protein prepd. from induced cultures
 CC of lambda RAL-1 lysogens recognise a single polypeptide of mol.
 CC wt. 42,000 in extracts of adult worms. Analysis deduced sequence
 CC suggests that it encodes a protein of mol. wt. 39,130. If the
 CC antigen is not subject to post-translational processing this
 CC suggests that most of the coding sequence is present. The three
 CC repeats are highly hydrophilic regions likely to be exposed on
 CC the surface of the antigen and highly immunogenic. Recombinant
 CC antigen expressed by the clone can be used stimulate T-cells of
 CC individuals infected by the parasite to proliferate and may be
 CC used as the basis for a vaccine against Onchocerciasis or river
 CC blindness.

XX CC

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: January 9, 2002, 15:01:18 : Search time 25.18 Seconds
(without alignments)
262.100 Million cell updates/sec

Title: US-09-828-000-3
Perfect score: 971
Sequence: 1 EPVAFKEQFLDGDGWTSM.....PDNTYEVKIDNSQVESGSLE 180

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 100059 seqs, 36664827 residues

Total number of hits satisfying chosen parameters: 100059

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_39:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	971	100.0	417	1	CRTC_HUMAN
2	933	96.1	416	1	CRTC_RAT
3	931	95.9	418	1	CRTC_RABIT
4	930	95.8	400	1	CRTL_BOVIN
5	930	95.8	416	1	CRTC_MOUSE
6	699	72.0	406	1	CRTC_DROME
7	664	68.4	388	1	RALI_ONCVO
8	619.5	63.8	395	1	CRTC_CABEL
9	537	55.3	424	1	CRTC_DICDI
10	535.5	55.1	401	1	CRTC_EUGGR
11	531	54.7	416	1	CRTC_BETVU
12	527	54.3	415	1	CRTC_RICCO
13	527	54.3	421	1	CRTC_PRUAR
14	527	54.3	424	1	CRTC_ORYSA
15	522.5	53.8	421	1	CRTL_BOVIN
16	522	53.8	416	1	CRTC_NICPL
17	518	53.3	424	1	CRTL_ARATH
18	512	52.7	420	1	CRTC_CHLRE
19	512	52.7	425	1	CRTL_ARATH
20	509	52.4	416	1	CRTC_BERST
21	504	51.9	393	1	CRTC_SCHMA
22	494	50.9	420	1	CRTC_MAIZE
23	455.5	46.9	424	1	CRTL_ARATH
24	447	46.0	105	1	CRTC_PIG
25	293	30.2	591	1	CALX_MOUSE
26	290	29.9	591	1	CALX_RAT
27	290	29.9	593	1	CALX_CANFA
28	288	29.7	592	1	CALX_HUMAN
29	270	27.8	611	1	CALG_MOUSE
30	261	26.9	610	1	CALG_HUMAN
31	253.5	26.1	560	1	CALX_SCHPO
32	244	25.1	619	1	CALX_CABEL
33	238.5	24.6	530	1	CAX1_ARATH

RESULT 1

ID	CRTC_HUMAN	STANDARD:	PRT:	417 AA.
AC	P27797;			
DT	01-AUG-1992 (Rel. 23, Created)			
DT	01-AUG-1992 (Rel. 23, Last sequence update)			
DT	20-AUG-2001 (Rel. 40, Last annotation update)			
DE	CALRETICULIN PRECURSOR (CRP55) (CALREGULIN) (HACBP) (ERP60) (52 KDA			
DE	RIBONUCLEOPROTEIN AUTOANTIGEN RO/SS-A).			
GN	CALR OR CRTC.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RP	MEDLINE=92013129; PubMed=1919005;			
RA	Rokeach L.A., Haselby J.A., Meilof J.F., Smeenk R.J., Unnasch T.R.,			
RA	Greene B.M., Hoch S.O.;			
RT	"Characterization of the autoantigen calreticulin.";			
RL	J. Immunol. 147:3031-3039(1991).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RP	MEDLINE=90237213; PubMed=2332496;			
RA	McCaulliffe D.P., Lux F.A., Lieu T.S., Sanz I., Hanke J., Newkirk M.M.,			
RA	Bachinski L.L., Itoh Y., Siciliano M.J., Reichlin M., Sontheimer R.D.,			
RA	Capra J.D.;			
RT	"Molecular cloning, expression, and chromosome 19 localization of a			
RT	human Ro/SS-A autoantigen.";			
RL	J. Clin. Invest. 85:1379-1391(1990).			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RP	MEDLINE=92129342; PubMed=1733953;			
RA	McCaulliffe D.P., Yang Y.S., Wilson J., Sontheimer R.D., Capra J.D.;			
RT	"The 5'-flanking region of the human calreticulin gene shares			
RT	homology with the human GRP78, GRP94, and protein disulfide isomerase			
RT	promoters.";			
RL	J. Biol. Chem. 267:2557-2562(1992).			
RN	[4]			
RP	SEQUENCE FROM N.A.			
RP	Lamerdin J., McCreedy P., Stillwagen S., Ramirez M., Carrano A.;			
RL	Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.			
RN	[5]			
RP	SEQUENCE OF 18-36.			
RP	MEDLINE=92002034; PubMed=1911778;			
RA	Rojiani M.V., Finlay B.B., Gray V., Dedhar S.;			
RT	"In vitro interaction of a polypeptide homologous to human Ro/SS-A			
RT	antigen (calreticulin) with a highly conserved amino acid sequence in			
RT	the cytoplasmic domain of integrin alpha subunits.";			
RL	Biochemistry 30:9859-9866(1991).			
RN	[6]			
RP	SEQUENCE OF 18-32.			
RP	MEDLINE=90380058; PubMed=2400400;			
RA	Krause K.H., Simmerman H.K.B., Jones L.R., Campbell K.P.;			
RT	"Sequence similarity of calreticulin with a Ca2(+)-binding protein			
RT	that co-purifies with an Ins(1,4,5)P3-sensitive Ca2+ store in HL-60			

34	232	23.9	546	1	CALX_SOYBN	Q39817 glycine max
35	215.5	22.2	540	1	CALX_HELTU	Q39994 helianthus
36	215.5	22.2	551	1	CALX_PEA	O82709 pisum sativ
37	202.5	20.9	528	1	CAX2_ARATH	Q35798 arabidopsis
38	133.5	13.7	502	1	CALX_YEAST	P27825 saccharomyc
39	86	8.9	24	1	CRTC_CANFA	P28490 canis famli
40	81	8.3	410	1	EFU_MESVI	Q9mup0 mesostigma
41	80.5	8.3	540	1	MTAL_ACICA	P25201 acinetobact
42	79.5	8.2	510	1	PROI_LISMO	P23224 listeria mo
43	78.5	8.1	344	1	ABIC_LACLA	Q01457 lactococcus
44	78	8.0	928	1	HXA2_HAEIN	P45354 haemophilus
45	77.5	8.0	659	1	AMIA_STRPN	P18791 streptococc

ALIGNMENTS

RT cells.";
 RL Biochem. J. 270:545-548(1990).
 [7]
 RN SEQUENCE OF 18-28.
 RP TISSUE: Liver;
 RX MEDLINE-93162045; PubMed 1286669;
 RA Hochstrasser D.F., Frutiger S., Paquet N., Bairoch A., Ravier F.,
 Pasquall C., Sanchez J.-C., Tissot J.-D., Bjellqvist B., Vargas R.,
 Appel R.D., Hughes G.J.;
 KA Human liver protein map: a reference database established by
 RT microsequencing and gel comparison.";
 RL Electrophoresis 13:992-1001(1992).
 [8]
 RN PARTIAL SEQUENCE OF 25-34; 56-62; 208-221 AND 273-278.
 RP TISSUE: Keratinocytes;
 RX MEDLINE-93162043; PubMed 1286667;
 RA Rasmussen H.H., van Damme J., Puype M., Gesser B., Celis J.E.,
 Vandekerckhove J.;
 RT "Microsequences of 145 proteins recorded in the two-dimensional gel
 RT protein database of normal human epidermal keratinocytes.";
 RL Electrophoresis 13:960-969(1992).
 [9]
 RN SEQUENCE OF 18-26.
 RP TISSUE: Colon carcinoma;
 RX MEDLINE-97295306; PubMed 9150948;
 RA Ji H., Reid G.E., Moritz R.L., Eddes J.S., Burgess A.W., Simpson R.J.;
 RT "A two-dimensional gel database of human colon carcinoma proteins.";
 RL Electrophoresis 18:605-613(1997).
 CC -!- FUNCTION: THIS PROTEIN BINDS CALCIUM. THERE ARE BOTH HIGH AND
 CC LOW AFFINITY CALCIUM-BINDING SITES.
 CC -!- SUBUNIT: MONOMER (BY SIMILARITY).
 CC -!- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM LUMEN.
 CC -!- SIMILARITY: BELONGS TO THE CALRETICULIN FAMILY.
 CC -!- CAUTION: WAS ORIGINALLY (REF.2) THOUGHT TO BE THE RO AUTOANTIGEN.
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 DR EMBL: M84739; AAA51916.1; -.
 DR EMBL: M32294; AAA36582.1; -.
 DR EMBL: AD000092; AAB51176.1; -.
 DR PIR: A37047; A37047.
 DR PIR: S11475; S11475.
 DR PIR: A42330; A42330.
 DR PIR: A46452; A46452.
 DR SWISS-2DPAGE: P27797; HUMAN.
 DR Arthur/Ghent-2DPAGE; 9401; IEF.
 DR HSC-2DPAGE; P27797; HUMAN.
 DR MIM: 109091; -.
 DR InterPro; IPR001580; Calreticulin.
 DR InterPro; IPR000886; ER target.
 DR Pfam; PF00262; calreticulin; 1.
 DR PRINTS; PR00626; CALRETICULIN.
 DR PRODOM; PD001866; Calreticulin; 1.
 DR PROSITE; PS00014; ER-TARGET; 1.
 DR PROSITE; PS00803; CALRETICULIN.1; 1.
 DR PROSITE; PS00804; CALRETICULIN.2; 1.
 DR PROSITE; PS00805; CALRETICULIN_REPEAT; 3.
 KW Endoplasmic reticulum; Calcium-binding; Repeat; Signal.
 FT SIGNAL
 FT CHAIN 1
 FT DOMAIN 18 417 CALRETICULIN.
 FT DOMAIN 18 197 P-DOMAIN.
 FT DOMAIN 198 308 C-DOMAIN.
 FT DOMAIN 309 417 C-DOMAIN.
 FT DOMAIN 191 255 4 X APPROXIMATE REPEATS.
 FT REPEAT 191 202 1-1.
 FT REPEAT 210 221 1-2.
 FT REPEAT 227 238 1-3.

FT REPEAT 244 255 1-4.
 FT DOMAIN 259 297 3 X APPROXIMATE REPEATS.
 FT REPEAT 259 269 2-1.
 FT REPEAT 273 283 2-2.
 FT REPEAT 287 297 2-3.
 FT DOMAIN 351 408 ASP/GLU/LYS-RICH.
 FT DISULFID 137 163 BY SIMILARITY.
 FT SITE 414 417 PREVENT SECRETION FROM ER.
 FT CONFLICT 35 35 MISSING (IN REF. 3).
 SQ SEQUENCE 417 AA; 48141 MW; BC37C3C0F1054FB2 CRC64;
 Query Match 100.0%; Score 971; DB 1; Length 417;
 Best Local Similarity 100.0%; Pred. No. 4.8e-80;
 Matches 180; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 EPAVYFKEQFLDGDGWTSRWIESKHKSDFGKFLVSSGKFYGDDEKDKGLQTSQDARFYAL 60
 DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 QY 18 EPAVYFKEQFLDGDGWTSRWIESKHKSDFGKFLVSSGKFYGDDEKDKGLQTSQDARFYAL 77
 DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 QY 61 SASPEPFSNKGQTLVVQFTVKHEQNIIDCGGYVVKLFPNSLDQTDHMDSEYNIMFGPDIC 120
 DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 QY 78 SASPEPFSNKGQTLVVQFTVKHEQNIIDCGGYVVKLFPNSLDQTDHMDSEYNIMFGPDIC 137
 DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 QY 121 GPCTKKVHVIFNYKGNVNLINKDIRCKDDEFTHLVTLVLRPONTYEVKIDNSQVSGSLE 180
 DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 QY 138 GPCTKKVHVIFNYKGNVNLINKDIRCKDDEFTHLVTLVLRPONTYEVKIDNSQVSGSLE 197
 DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 RESULT 2
 CRTC_RAT
 ID CRTC_RAT STANDARD; PRT; 416 AA.
 AC P18418; P10452;
 DT 01-MAR-1989 (Rel. 10, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE CALRETICULIN PRECURSOR (CRP55) (CALREGULIN) (HACBP) (ERP60) (CALBP)
 DE (CALCIUM-BINDING PROTEIN 3) (CABP3).
 GN CALR.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
 OX NCBI_TaxID-10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX STRAIN-SPRAGUE-DAWLEY; TISSUE-Brain cortex;
 RX MEDLINE-90370496; PubMed-2395661;
 RA Murthy K.K., Bonville D., Srikanth C.B., Carrier F., Bell A.,
 RA Holmes C., Patel Y.C.;
 RT "Structural homology between the rat calreticulin gene product and
 RT the Onchocerca volvulus antigen Ral-1.";
 RL Nucleic Acids Res. 18:4933-4933(1990).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX STRAIN-SPRAGUE-DAWLEY;
 RX MEDLINE-93202172; PubMed-8453984;
 RA Nakamura M., Moriya M., Baba T., Michikawa Y., Yamanobe T., Arai K.,
 RA Okinaga S., Kobayashi T.;
 RT "An endoplasmic reticulum protein, calreticulin, is transported into
 RT the acrosome of rat sperm.";
 RL Exp. Cell Res. 205:101-110(1993).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX STRAIN SPRAGUE-DAWLEY; TISSUE-Liver;
 RX MEDLINE-95181573; PubMed-7876339;
 RA Soennichsen B., Fueflekrug J., van Nguyen P., Diekmann W.,
 RA Robinson D.G., Mieskes G.;
 RT "Retention and retrieval: both mechanisms cooperate to maintain
 RT calreticulin in the endoplasmic reticulum.";
 RL J. Cell Sci. 107:2705-2717(1994).
 RN [4]
 RP SEQUENCE OF 270-358 FROM N.A.
 RX STRAIN-SPRAGUE-DAWLEY;

RA Lone Y.C., Bailly A., Latruffe N.;
 RL Submitted (DEC-1988) to the EMBL/GenBank/DBJ databases.
 RN (5)
 RP SEQUENCE OF 18-29.
 RX MEDLINE=91054414; PubMed=2241926;
 RA Treves S., de Mattei M., Lanfredi M., Villa A., Green N.M.,
 RA MacIennan D.H., Meldolesi J., Pozzan T.;
 RT "Calreticulin is a candidate for a calsequestrin-like function in
 RT Ca2(+)-storage compartments (calciosomes) of liver and brain.";
 RL Biochem. J. 271:473-480(1990).
 RN (6)
 RP SEQUENCE OF 18-32.
 RC STRAIN=SPRAGUE-DAWLEY; TISSUE=Testis;
 RX MEDLINE=92360010; PubMed=1497655;
 RA Nakamura M., Michikawa Y., Baba T., Okinaga S., Arai K.;
 RT "Calreticulin is present in the acrosome of spermatids of rat
 RT testis.";
 RL Biochem. Biophys. Res. Commun. 186:668-673(1992).
 RN (7)
 RP SEQUENCE OF 18-32.
 RC STRAIN=LEC; TISSUE=Liver;
 RX MEDLINE=94072621; PubMed=8251535;
 RA Yokoi T., Nagayama S., Kajiwara R., Kawaguchi Y., Horiuchi R.,
 RA Kamataki T.;
 RT "Identification of protein disulfide isomerase and calreticulin as
 RT autoantigenic antigens in LEC strain of rats.";
 RL Biochim. Biophys. Acta 1158:339-344(1993).
 CC -!- FUNCTION: THIS PROTEIN BINDS CALCIUM. THERE ARE BOTH HIGH AND
 CC LOW AFFINITY CALCIUM-BINDING SITES.
 CC -!- SUBUNIT: MONOMER (BY SIMILARITY).
 CC -!- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM LUMEN.
 CC -!- SIMILARITY: BELONGS TO THE CALRETICULIN FAMILY.
 CC -!- CAUTION: WAS ORIGINALLY (REF.2) THOUGHT TO BE D-BETA-
 CC HYDROXYBUTYRATE DEHYDROGENASE.
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 DR EMBL; D78308; BAA11345.1; -;
 DR EMBL; X53363; CAA37446.1; -;
 DR EMBL; X13702; CAA31987.1; ALT_SEQ.
 DR EMBL; X79327; CAA55890.1; -;
 DR PIR; S04867; S04867.
 DR PIR; S11205; S11205.
 DR PIR; S13045; S13045.
 DR PIR; A49176; A49176.
 DR PIR; S45036; S45036.
 DR PIR; JH0819; JH0819.
 DR InterPro; IPR001580; Calreticulin.
 DR InterPro; IPR000886; ER_target.
 DR Pfam; PF00262; calreticulin; 1.
 DR PRINTS; PR00626; CALRETICULIN.
 DR ProDom; PD001866; Calreticulin; 1.
 DR PROSITE; PS00014; ER_TARGET; 1.
 DR PROSITE; PS00803; CALRETICULIN_1; 1.
 DR PROSITE; PS00804; CALRETICULIN_2; 1.
 DR PROSITE; PS00805; CALRETICULIN_REPEAT; 3.
 DR Endoplasmic reticulum; Calcium-binding; Repeat; Signal.
 FT SIGNAL 1 17
 FT CHAIN 18 416 CALRETICULIN.
 FT DOMAIN 18 197 N-DOMAIN.
 FT DOMAIN 198 308 P-DOMAIN.
 FT DOMAIN 309 416 C-DOMAIN.
 FT DOMAIN 191 255 4 X APPROXIMATE REPEATS.
 FT REPEAT 191 202 1-1.
 FT REPEAT 210 221 1-2.
 FT REPEAT 227 238 1-3.
 FT REPEAT 244 255 1-4.

FT DOMAIN 259 297 3 X APPROXIMATE REPEATS.
 FT REPEAT 259 269 2-1.
 FT REPEAT 273 283 2-2.
 FT REPEAT 287 297 2-3.
 FT DOMAIN 351 407 ASP/GLU/LYS-RICH.
 FT DISULFID 137 163 BY SIMILARITY.
 FT SITE 413 416 PREVENT SECRETION FROM ER.
 SQ SEQUENCE 416 AA; 47995 MW; 256713CED31A2970 CRC64;
 Query Match 96.1%; Score 933; DB 1; Length 416;
 Best Local Similarity 94.4%; Pred. No. 1.2e-76;
 Matches 170; Conservative 5; Mismatches 5; Indels 0; Gaps 0;
 Qy 1 EPAYVFEQFLDGDGWTSRWIESKHSDFGKFLVSSGKFGYGDDEKDKGLQTSQDARFYAL 60
 :||:||||||| ||:||||||| ||:||||||| ||:||||||| ||:||||||| ||:|||||||
 Db 18 DPATVFEQFLDGDGDAWNTNRWESKHSDFGKFLVSSGKFGYGDDEKDKGLQTSQDARFYAL 77
 Qy 61 SASPEPFSNKGQTLVVQFTVKHEQNIIDCGGGYVKLFPNLSLQDTMHGDSSEYNIMFGPDIC 120
 || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 78 SARPEPFSNKGQTLVVQFTVKHEQNIIDCGGGYVKLFPNLSLQDTMHGDSSEYNIMFGPDIC 137
 Qy 121 GPGTKKVVHVIENYKGNVLIINKDIRCKDDETHLTVLRPDNTVEVKIDNSQVSGSLE 180
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 138 GPGTKKVVHVIENYKGNVLIINKDIRCKDDETHLTVLRPDNTVEVKIDNSQVSGSLE 197
 RESULT 3
 ID CRTG_RABIT STANDARD; PRT; 418 AA.
 AC P15253;
 DT 01-APR-1990 (Rel. 14, Created)
 DT 01-APR-1990 (Rel. 14, Last sequence update)
 DT 01-OCT-1996 (Rel. 34, Last annotation update)
 DE CALRETICULIN PRECURSOR (CRP55) (CALREGULIN) (HACBP) (ERP60).
 GN CALR.
 OS Oryctolagus cuniculus (Rabbit).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
 OX NCBI_TaxID=9986;
 RN [1]
 RC SEQUENCE FROM N.A.
 RP TISSUE=Slow-twitch skeletal muscle;
 RX MEDLINE=90094320; PubMed=2600080;
 RA Fliegel L., Burns K., MacIennan D.H., Reithmeier R.A.F., Michalak M.;
 RT "Molecular cloning of the high affinity calcium-binding protein
 RT (calreticulin) of skeletal muscle sarcoplasmic reticulum.";
 RL J. Biol. Chem. 264:21522-21528(1989).
 RN [2]
 RC SEQUENCE FROM N.A.
 RP TISSUE=Fast-twitch skeletal muscle;
 RX MEDLINE=91282795; PubMed=2059224;
 RA Fliegel L., Michalak M.;
 RT "Fast-twitch and slow-twitch skeletal muscles express the same
 RT isoform of calreticulin.";
 RL Biochem. Biophys. Res. Commun. 177:979-984(1991).
 RN [3]
 RC SEQUENCE OF 18-36.
 RX MEDLINE=91054414; PubMed=2241926;
 RA Treves S., de Mattei M., Lanfredi M., Villa A., Green N.M.,
 RA MacIennan D.H., Meldolesi J., Pozzan T.;
 RT "Calreticulin is a candidate for a calsequestrin-like function in
 RT Ca2(+)-storage compartments (calciosomes) of liver and brain.";
 RL Biochem. J. 271:473-480(1990).
 RN [4]
 RP SEQUENCE OF 18-46.
 RX MEDLINE=91201375; PubMed=2016321;
 RA Milner R.E., Baksh S., Shemanko C., Carpenter M.R., Smillie L.,
 RA Vance J.E., Opas M., Michalak M.;
 RT "Calreticulin, and not calsequestrin, is the major calcium binding
 RT protein of smooth muscle sarcoplasmic reticulum and liver endoplasmic
 RT reticulum.";
 RL J. Biol. Chem. 266:7155-7165(1991).

RR PARTIAL SEQUENCE.
RC TISSUE: Lung;
RX MEDLINE-94002038; PubMed 1911780;
RT Guan S., Fallick A.M., Williams D.E., Cashman J.R.;
"Evidence for complex formation between rabbit lung flavin-containing
monooxygenase and calreticulin."
RL Biochemistry 30:9892-9900(1991).
CC -|- FUNCTION: THIS PROTEIN BINDS CALCIUM. THERE ARE BOTH HIGH AND
CC LOW AFFINITY CALCIUM-BINDING SITES.
CC -|- SUBUNIT: MONOMER (BY SIMILARITY).
CC -|- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM LUMEN.
CC -|- SIMILARITY: BELONGS TO THE CALRETICULIN FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; J05138; AAA31188.1; -;
DR PIR; A34154; A34154.
DR PIR; C33208; C33208.
DR PIR; D33208; D33208.
DR PIR; E33208; E33208.
DR PIR; F33208; F33208.
DR PIR; S13046; S13046.
DR PIR; S13047; S13047.
DR InterPro; IPR001580; Calreticulin.
DR InterPro; IPR000886; ER-target.
DR Pfam; PF00262; calreticulin; 1.
DR PRINTS; PR00626; CALRETICULIN.
DR PRODOM; PD001866; Calreticulin; 1.
DR PROSITE; PS00014; ER-TARGET; 1.
DR PROSITE; PS00803; CALRETICULIN_1; 1.
DR PROSITE; PS00804; CALRETICULIN_2; 1.
DR PROSITE; PS00805; CALRETICULIN_REPEAT; 3.
KW Endoplasmic reticulum; Calcium-binding; Repeat; Signal.
FT SIGNAL 1 17
FT CHAIN 18 418 CALRETICULIN.
FT DOMAIN 18 197 N-DOMAIN.
FT DOMAIN 198 308 P-DOMAIN.
FT DOMAIN 309 418 C-DOMAIN.
FT DOMAIN 191 255 4 X APPROXIMATE REPEATS.
FT REPEAT 191 202 1-1.
FT REPEAT 210 221 1-2.
FT REPEAT 220 238 1-3.
FT REPEAT 244 255 1-4.
FT REPEAT 259 297 3 X APPROXIMATE REPEATS.
FT REPEAT 259 269 2-1.
FT REPEAT 273 283 2-2.
FT REPEAT 287 297 2-3.
FT DOMAIN 351 408 ASP/GLU/LYS-RICH.
FT DISULFID 137 163 BY SIMILARITY.
FT SITE 415 418 PREVENT SECRETION FROM ER.
FT VARIANT 35 35 E -> D.
FT CONFLICT 90 90 P -> T (IN REF. 5).
SQ SEQUENCE 418 AA; 48275 MW; B6082B689DC763A6 CRC64;

Query Match 95.9%; Score 931; DB 1; Length 418;
Best Local Similarity 95.6%; Pred. No. 1.9e-76;
Matches 172; Conservative 1; Mismatches 7; Indels 0; Gaps 0;
QY 1 EPVAVYFKQFLDGDGWTGRWIESKHKSDFGKFLVSSGKFGYGDDEKDKGLQTSQDARFYAL 60
DB 18 EPVAVYFKQFLDGDGWTGRWIESKHKSDFGKFLVSSGKFGYGDDEKDKGLQTSQDARFYAL 77
QY 61 SASFPFPNKGQTLVQFTVKHEQNDICGGGVYKFLFPNSLDQTDHMGSEYNIMEGPDIC 120
DB 78 SARFPFPNKGQTLVQFTVKHEQNDICGGGVYKFLFPNSLDQTDHMGSEYNIMEGPDIC 137

QY 121 GPGTKKVVHFIENYKGNVLIINKDIRKDDFTHLYTLIVRPDNTYEVKIDNSQVSGSLE 180
DB 138 GPGTKKVVHFIENYKGNVLIINKDIRKDDFTHLYTLIVRPDNTYEVKIDNSQVSGSLE 197
RESULT 4
CRT1_BOVIN
ID CRT1_BOVIN STANDARD; PRT; 400 AA.
AC P52193;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE CALRETICULIN, BRAIN ISOFORM 1 (CRP55) (CALREGULIN) (HACBP).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID:9913;
RN [1]
RP SEQUENCE.
RC TISSUE: Brain;
RX MEDLINE-94183174; PubMed 8135753;
RA Matsuo K., Seta K., Yamakawa Y., Okuyama T., Shinoda T.;
RT "Covalent structure of bovine brain calreticulin";
RL Biochem. J. 298:435-442(1994).
CC -|- FUNCTION: THIS PROTEIN BINDS CALCIUM. THERE ARE BOTH HIGH AND
CC LOW AFFINITY CALCIUM-BINDING SITES.
CC -|- SUBUNIT: MONOMER.
CC -|- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM LUMEN.
CC -|- SIMILARITY: BELONGS TO THE CALRETICULIN FAMILY.
DR InterPro; IPR001580; Calreticulin.
DR InterPro; IPR000886; ER-target.
DR Pfam; PF00262; calreticulin; 1.
DR PRINTS; PR00626; CALRETICULIN.
DR PRODOM; PD001866; Calreticulin; 1.
DR PROSITE; PS00014; ER-TARGET; 1.
DR PROSITE; PS00803; CALRETICULIN_1; 1.
DR PROSITE; PS00804; CALRETICULIN_2; 1.
DR PROSITE; PS00805; CALRETICULIN_REPEAT; 3.
KW Endoplasmic reticulum; Calcium-binding; Repeat; Glycoprotein.
FT DOMAIN 1 180 N-DOMAIN.
FT DOMAIN 181 291 P-DOMAIN.
FT DOMAIN 292 400 C-DOMAIN.
FT DOMAIN 174 238 4 X APPROXIMATE REPEATS.
FT REPEAT 174 185 1-1.
FT REPEAT 193 204 1-2.
FT REPEAT 210 221 1-3.
FT REPEAT 227 238 1-4.
FT DOMAIN 242 280 3 X APPROXIMATE REPEATS.
FT REPEAT 242 252 2-1.
FT REPEAT 256 266 2-2.
FT REPEAT 270 280 2-3.
FT DOMAIN 334 390 ASP/GLU/LYS-RICH.
FT DISULFID 120 146 N-LINKED (GLCNAC...).
FT CARBOHYD 162 162 PREVENT SECRETION FROM ER (POTENTIAL).
FT SITE 397 400
SQ SEQUENCE 400 AA; 46381 MW; 7D4B68DFC689EEF1 CRC64;

Query Match 95.8%; Score 930; DB 1; Length 400;
Best Local Similarity 95.0%; Pred. No. 2.2e-76;
Matches 171; Conservative 3; Mismatches 6; Indels 0; Gaps 0;
QY 1 EPVAVYFKQFLDGDGWTGRWIESKHKSDFGKFLVSSGKFGYGDDEKDKGLQTSQDARFYAL 60
DB 1 DPTVYFKQFLDGDGWTGRWIESKHKSDFGKFLVSSGKFGYGDDEKDKGLQTSQDARFYAL 60
QY 61 SASFPFPNKGQTLVQFTVKHEQNDICGGGVYKFLFPNSLDQTDHMGSEYNIMEGPDIC 120
DB 61 SARFPFPNKGQTLVQFTVKHEQNDICGGGVYKFLFPNSLDQTDHMGSEYNIMEGPDIC 120
QY 121 GPGTKKVVHFIENYKGNVLIINKDIRKDDFTHLYTLIVRPDNTYEVKIDNSQVSGSLE 180


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Db 121 GPGTKKVVHVIENYKGNVLINRCKDDETHLYTLVRPNTYEVKIDNSQVSSGLE 180
|||||
RESULT 5
ID CRTC_MOUSE STANDARD; PRT; 416 AA.
AC P14211;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE CALRETICULIN PRECURSOR (CRP55) (CALREGULIN) (HACBP) (ERP60).
GN CALR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 18-48 AND 129-161.
RC STRAIN=BALB/C; TISSUE=Liver;
RA MEDLINE=90059955; PubMed=2583110;
RX Smith M.J., Koch G.L.E.;
RT "Multiple zones in the sequence of calreticulin (CRP55, calregulin,
RL HACBP), a major calcium binding ER/SR protein.";
RL EMBO J. 8:3581-3586(1989).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=93013037; PubMed=1398135;
RA Mazzarella R.A., Gold P., Cunningham M., Green M.;
RT "Determination of the sequence of an expressible cDNA clone encoding
RP60/calregulin by the use of a novel nested set method.";
RL Gene 120:217-225(1992).
RN [3]
RP SEQUENCE OF 18-38.
RC TISSUE=Fibroblast;
RX MEDLINE=95009907; PubMed=7523108;
RA Merrick B.A., Patterson R.M., Wichter L.L., He C., Selkirk J.K.;
RT "Separation and sequencing of familial and novel murine proteins
using preparative two-dimensional gel electrophoresis.";
RL Electrophoresis 15:735-745(1994).
CC -1- FUNCTION: THIS PROTEIN BINDS CALCIUM. THERE ARE BOTH HIGH AND
CC LOW AFFINITY CALCIUM-BINDING SITES.
CC -1- SUBUNIT: MONOMER (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM LUMEN.
CC -1- SIMILARITY: BELONGS TO THE CALRETICULIN FAMILY.
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DR EMBL; X14926; CAA33053.1; -;
DR EMBL; M92988; AAA37569.1; -;
DR PIR; S06763; S06763.
DR PIR; JC1444; JC1444.
DR SWISS-2DPAGE; P14211; MOUSE.
DR MGD; MGI-88252; Calr.
DR InterPro; IPR001580; Calreticulin.
DR InterPro; IPR000886; ER target.
DR Pfam; PF00262; calreticulin; 1.
DR PRINTS; PR00626; CALRETICULIN.
DR PRODom; PD001866; Calreticulin; 1.
DR PROSITE; PS00014; ER_TARGET; 1.
DR PROSITE; PS00803; CALRETICULIN_1; 1.
DR PROSITE; PS00804; CALRETICULIN_2; 1.
DR PROSITE; PS00805; CALRETICULIN_REPEAT; 3.
KW Endoplasmic reticulum; Calcium-binding; Repeat; Signal.
FT SIGNAL 1 17
FT CHAIN 18 416 CALRETICULIN.
FT DOMAIN 18 197 N-DOMAIN.

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FT DOMAIN 198 308 P-DOMAIN.
FT DOMAIN 309 416 C-DOMAIN.
FT DOMAIN 417 416 4 X APPROXIMATE REPEATS.
FT REPEAT 191 255 1-1.
FT REPEAT 191 202 1-1.
FT REPEAT 210 221 1-2.
FT REPEAT 227 238 1-3.
FT REPEAT 244 255 1-4.
FT DOMAIN 259 297 3 X APPROXIMATE REPEATS.
FT REPEAT 259 269 2-1.
FT REPEAT 273 283 2-2.
FT REPEAT 287 297 2-3.
FT DOMAIN 351 407 ASP/GLU/LYS-RICH.
FT DISULFID 137 163 BY SIMILARITY.
FT SITE 413 416 PREVENT SECRETION FROM ER.
SQ SEQUENCE 416 AA; 47994 MW; 24C03B00913408D8 CRC64;

Query Match 95.8%; Score 930; DB 1; Length 416;
Best Local Similarity 94.4%; Pred. No. 2.3e-76;
Matches 170; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

Qy 1 BPAVYFKEQFLDGDGWTSRWIESKHKSDFGVLSGGKFYGDDEKDKGLQTSQDARFYAL 60
Db 18 DPAYFKEQFLDGDGWTNRWVESKHKSDFGVLSGGKFYGDLEKDKGLQTSQDARFYAL 77

Qy 61 SASPEPFSNKGQTLVVOFTVKHEQNDICGGGYVVKLPFNSLDQTDHMGDSEYNIMFGPDIC 120
Db 78 SAKPEPFSNKGQTLVVOFTVKHEQNDICGGGYVVKLPFNSLDQTDHMGDSEYNIMFGPDIC 137

Qy 121 GPGTKKVVHVIENYKGNVLINRCKDDETHLYTLVRPNTYEVKIDNSQVSSGLE 180
Db 138 GPGTKKVVHVIENYKGNVLINRCKDDETHLYTLVRPNTYEVKIDNSQVSSGLE 197

RESULT 6
ID CRTC_MOUSE STANDARD; PRT; 406 AA.
AC P29413; OSVHA3;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-OCT-1993 (Rel. 27, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE CALRETICULIN PRECURSOR (CRP55) (CALREGULIN) (HACBP).
GN CRC OR CG9429.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93208374; PubMed=1296819;
RA Smith M.J.;
RT "Nucleotide sequence of a Drosophila melanogaster gene encoding a
RL calreticulin homologue.";
RL DNA Seq. 3:247-250(1992).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=BERKELEY;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,

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FT REPEAT 211 222 1-2.
FT REPEAT 227 238 1-3.
FT REPEAT 246 257 1-4.
FT DOMAIN 260 298 3 X 11 AA APPROXIMATE REPEATS.
FT REPEAT 260 270 2-1.
FT REPEAT 274 284 2-2.
FT REPEAT 288 298 2-3.
FT DISULFID 105 137 BY SIMILARITY.
FT SITE 421 424 PREVENT SECRETION FROM ER (POTENTIAL).
SQ SEQUENCE 424 AA: 48350 MW; BAP273694FB6FC37 CRC64;

Query Match 55.3%; Score 537; DB 1; Length 424;
Best Local Similarity 57.2%; Pred. No. 4.7e-41;
Matches 103; Conservative 36; Mismatches 33; Indels 8; Gaps 7;

QY 4 VYFKEFLDGDGWTWSWIESK-HKSD--FGKFLSSGKFGDEEDKGLQTSODARFYAL 60
DB 21 VHPKDTF-DND-WESRWVSDMHKEDGSKGLVHTAGKWFGENQ-KGIQTSEDARFYAV 77
QY 61 SASFEPENKGGOTLVQFTVKHEQNDICGGYVVKLPNSLDQTDHMGDSEYNIMFGPDIC 120
DB 78 SAKFSPSNKGLVQYTVKNEQKVDCCGYSIKLLPSKLDQSAFDGSESEYSIMFGPDVC 137
QY 121 GPCTKKVHVIFNYKGNVLINKDI-RCKDDEFTHLVTLVIRPDPNTVEVKIDNSQVESGSL 179
DB 138 G-ASKRVHVLNKGKHLIKKEINKVETDQLTHQYTLVISPDPNTYVNLVDNKEIQAGNL 196

RESULT 10
CRTC_EUGGR
ID CRTC_EUGGR STANDARD; PRT; 401 AA.
AC Q92NY3;
DT 20-AUG-2001 (Rel. 40, Created)
DT 20-AUG-2001 (Rel. 40, Last sequence update)
DE CALRETICULIN PRECURSOR.
OS Euglena gracilis.
OC Eukaryota; Euglenozoa; Euglenida; Euglenales; Euglena.
OX NCBI_TaxID 3039;
RN [1]
SEQUENCE FROM N.A.
RA Navaziz L., Balidan B., Martin W., Mariani P.;
RT "Evidence for conservation of a calcium homeostat component: purification characterization and cloning of calreticulin from Euglena gracilis.";
RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: THIS PROTEIN BINDS CALCIUM. THERE ARE BOTH HIGH AND LOW AFFINITY CALCIUM-BINDING SITES (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM LUMEN (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE CALRETICULIN FAMILY.
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CC
CC EMBL; Y09816; CAA70945.1;
DR InterPro; IPR001580; Calreticulin.
DR InterPro; IPR000886; ER-target.
DR Pfam; PF00262; calreticulin; 1.
DR PRINTS; P000626; CALRETICULIN.
DR PRODOM; PD001866; Calreticulin; 1.
DR PROSITE; PS00014; ER-TARGET; 1.
DR PROSITE; PS00803; CALRETICULIN_1; 1.
DR PROSITE; PS00804; CALRETICULIN_2; 1.
DR PROSITE; PS00805; CALRETICULIN_REPEAT; 1.
KW Endoplasmic reticulum; Calcium-binding; Repeat; Signal.
FT SIGNAL 1 18 POTENTIAL.
FT CHAIN 19 401 CALRETICULIN.
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FT SITE 398 401 PREVENT SECRETION FROM ER (POTENTIAL).
SQ SEQUENCE 401 AA: 45910 MW; 056B074C16292674 CRC64;

Query Match 55.1%; Score 535.5; DB 1; Length 401;
Best Local Similarity 56.7%; Pred. No. 6e-41;
Matches 101; Conservative 30; Mismatches 42; Indels 5; Gaps 4;

QY 4 VYFKEFLDGDGWTWSWIESKHKSDFGKFLSSGKFGDEEDKGLQTSODARFYALSAS 63
DB 20 IYKETF--EPDWETRWTHSTAKSDYKFKLTSGKFGDKAKDAGIQTSDAKFYAISP 77
QY 64 F-EPPFNKGGOTLVQFTVKHEQNDICGGYVVKLPNSLDQTDHMGDSEYNIMFGPDICGP 122
DB 78 IASSFNEGKDLVQLQFSVHEQDIDCGGYLKLLP-SVDAAKFTGTPPHIIFGPDICG- 135
QY 123 GTRKKVHVIFNYKGNVLINKDI-RCKDDEFTHLVTLVIRPDPNTVEVKIDNSQVESGSL 180
DB 136 ATKKIHFILTYKGNLLKKPRCETDTLSHTVTAVIKADRTVEVLVDQVKKESGTL 193

RESULT 11
CRTC_BETVU
ID CRTC_BETVU STANDARD; PRT; 416 AA.
AC O81919;
DT 20-AUG-2001 (Rel. 40, Created)
DT 20-AUG-2001 (Rel. 40, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE CALRETICULIN PRECURSOR.
OS Beta vulgaris (Sugar beet).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Caryophyllidae; Caryophyllales; Chenopodiaceae; Beta.
OX NCBI_TaxID 3555;
RN [1]
SEQUENCE FROM N.A.
RC STRAIN-VV-D/2R5; TISSUE=Leaf;
RA Viereck R.;
RT "Nucleotide sequence from sugar beet calreticulin.";
RL Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: THIS PROTEIN BINDS CALCIUM. THERE ARE BOTH HIGH AND LOW AFFINITY CALCIUM-BINDING SITES (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM LUMEN (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE CALRETICULIN FAMILY.
CC
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CC
CC EMBL; AJ002057; CAA05161.1;
DR Mendel; 32549; Betvu.1166;32549
DR InterPro; IPR001580; Calreticulin.
DR InterPro; IPR000886; ER-target.
DR Pfam; PF00262; calreticulin; 1.
DR PRINTS; P000626; CALRETICULIN.
DR PRODOM; PD001866; Calreticulin; 1.
DR PROSITE; PS00014; ER-TARGET; 1.
DR PROSITE; PS00803; CALRETICULIN_1; 1.
DR PROSITE; PS00804; CALRETICULIN_2; 1.
DR PROSITE; PS00805; CALRETICULIN_REPEAT; 2.
KW Endoplasmic reticulum; Calcium-binding; Repeat; Signal; Glycoprotein.
FT SIGNAL 1 25 POTENTIAL.
FT CHAIN 26 416 CALRETICULIN.
FT CARBOHYD 57 57 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 157 157 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT SITE 413 416 PREVENT SECRETION FROM ER (POTENTIAL).
SQ SEQUENCE 416 AA: 48136 MW; 565FEC3489F77CA7 CRC64;
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Query Match 54.7%; Score 531; DB 1; Length 416;
Best Local Similarity 55.9%; Pred. No. 1.6e-40;
Matches 100; Conservative 28; Mismatches 45; Indels 6; Gaps 3;

Qy 4 VFKEQFLDGGWTSRWIESKHSD---FGKFLVSSGKFGYDEEKDKGLQTSQDARFYAL 60
   |||:|:| ||| |||:|:| |||:|:| |||:|:| |||:|:| |||:|:| |||:|:|
Db 27 VFEEERF--EDGWRKWKSEKWDKESWAGWNYTSGKNGD-AMDKGIQTSERYFYAI 83
   |||:|:| ||| |||:|:| |||:|:| |||:|:| |||:|:| |||:|:| |||:|:|
Qy 61 SASPEFPFNKGGTLLVQVTVKHEQNIIDCGGKLVKLPNSLDQTMHGDSEYNIMFGPDIC 120
   |||:|:| ||| |||:|:| |||:|:| |||:|:| |||:|:| |||:|:| |||:|:|
Db 84 SAERPEFSNKDNTLVFQFSVKEHQKLDGCGGKLVKLPNSLDQTMHGDSEYNIMFGPDIC 143
   |||:|:| ||| |||:|:| |||:|:| |||:|:| |||:|:| |||:|:| |||:|:|
Qy 121 GPGTKKVVHINYGKKNVLIINKDRCKDETHLYTLVRPDNTVEYKIDNSQVSGSL 179
   |||:|:| ||| |||:|:| |||:|:| |||:|:| |||:|:| |||:|:| |||:|:|
Db 144 GYSTKKVHAIFNYNDTNHLIKKVPCETDQLTHVTVTLRDPDATYSILIDNKEQKOTGSL 202
   |||:|:| ||| |||:|:| |||:|:| |||:|:| |||:|:| |||:|:| |||:|:|

RESULT 12
CRTC_RICCO STANDARD; PRT; 415 AA.
ID CRTC_RICCO AC P93508;
DT 20-AUG-2001 (Rel. 40, Created)
DT 20-AUG-2001 (Rel. 40, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE CALRETICULIN PRECURSOR.
OS Ricinus communis (Castor bean).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids I; Malpighiales; Euphorbiaceae; Ricinus.
OX NCBI_TaxID=3988;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97435975; PubMed=9290642;
RA Coughlan S.J., Hastings C., Winfrey R. Jr.;
RT "Cloning and characterization of the calreticulin gene from Ricinus
  communis L.";
RL Plant Mol. Biol. 34:897-911(1997).
CC -!- FUNCTION: THIS PROTEIN BINDS CALCIUM. THERE ARE BOTH HIGH AND
  LOW AFFINITY CALCIUM-BINDING SITES.
CC -!- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM LUMEN.
CC -!- SIMILARITY: BELONGS TO THE CALRETICULIN FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
  between the Swiss Institute of Bioinformatics and the EMBL outstation -
  the European Bioinformatics Institute. There are no restrictions on its
  use by non-profit institutions as long as its content is in no way
  modified and this statement is not removed. Usage by and for commercial
  entities requires a license agreement (See http://www.isb-sib.ch/announce/
  or send an email to license@isb-sib.ch).
CC -----
DR EMBL; U74631; AAB71420.1; -
DR EMBL; U74630; AAB71419.1; -
DR Mendel; 10452; Ricco;1166;10452.
DR InterPro; IPR001580; Calreticulin.
DR InterPro; IPR000886; ER_target.
DR Pfam; PF00262; calreticulin; 1.
DR PRINTS; PR00626; CALRETICULIN.
DR PRODOM; PD001866; Calreticulin; 1.
DR PROSITE; PS00014; ER_TARGET; 1.
DR PROSITE; PS00803; CALRETICULIN_1; 1.
DR PROSITE; PS00804; CALRETICULIN_2; 1.
DR PROSITE; PS00805; CALRETICULIN_REPEAT; 2.
KW Endoplasmic reticulum; Calcium-binding; Repeat; Signal; Glycoprotein.
FT SIGNAL 1 20 POTENTIAL.
FT CHAIN 21 415 CALRETICULIN.
FT CARBOHYD 52 52 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 152 152 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT SITE 412 415 PREVENT SECRETION FROM ER (POTENTIAL).
SQ SEQUENCE 415 AA; 47522 MW; DD5F452E76CC7F8C CRC64;

Query Match 54.3%; Score 527; DB 1; Length 415;
Best Local Similarity 55.3%; Pred. No. 3.6e-40;
Matches 99; Conservative 28; Mismatches 46; Indels 6; Gaps 3;
```

```
Matches 99; Conservative 31; Mismatches 43; Indels 6; Gaps 3;

Qy 4 VFKEQFLDGGWTSRWIESKHSD---FGKFLVSSGKFGYDEEKDKGLQTSQDARFYAL 60
   |||:|:| ||| |||:|:| |||:|:| |||:|:| |||:|:| |||:|:| |||:|:|
Db 22 VFEEERF--EDGWRKWKSDMKKDGNTAGWNYTSGKNGD-PNDKGIQTSERYFYAI 78
   |||:|:| ||| |||:|:| |||:|:| |||:|:| |||:|:| |||:|:| |||:|:|
Qy 61 SASPEFPFNKGGTLLVQVTVKHEQNIIDCGGKLVKLPNSLDQTMHGDSEYNIMFGPDIC 120
   |||:|:| ||| |||:|:| |||:|:| |||:|:| |||:|:| |||:|:| |||:|:|
Db 79 SAERPEFSNKDNTLVFQFSVKEHQKLDGCGGKLVKLPNSLDQTMHGDSEYNIMFGPDIC 138
   |||:|:| ||| |||:|:| |||:|:| |||:|:| |||:|:| |||:|:| |||:|:|
Qy 121 GPGTKKVVHINYGKKNVLIINKDRCKDETHLYTLVRPDNTVEYKIDNSQVSGSL 179
   |||:|:| ||| |||:|:| |||:|:| |||:|:| |||:|:| |||:|:| |||:|:|
Db 139 GYSTKKVHAIFNYNDTNHLIKKVPCETDQLTHVTVTLRDPDATYSILIDNKEQKOTGSL 197
   |||:|:| ||| |||:|:| |||:|:| |||:|:| |||:|:| |||:|:| |||:|:|

RESULT 13
CRTC_PRUAR STANDARD; PRT; 421 AA.
ID CRTC_PRUAR AC Q9XF98;
DT 20-AUG-2001 (Rel. 40, Created)
DT 20-AUG-2001 (Rel. 40, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE CALRETICULIN PRECURSOR.
OS Prunus armeniaca (Apricot).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids I; Rosales; Rosaceae; Prunus.
OX NCBI_TaxID=36596;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. BERGERON; TISSUE=Mesocarp, and Endocarp;
RA Mbeugue-A-Mbeugue D., Fills-Lycaon B.R.;
RT "Molecular cloning and nucleotide sequence of a calreticulin from
  apricot (Prunus armeniaca cv. Bergeron)";
RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: THIS PROTEIN BINDS CALCIUM. THERE ARE BOTH HIGH AND
  LOW AFFINITY CALCIUM-BINDING SITES (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM LUMEN (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE CALRETICULIN FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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  the European Bioinformatics Institute. There are no restrictions on its
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  entities requires a license agreement (See http://www.isb-sib.ch/announce/
  or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AF134733; AAD32207.1; -
DR InterPro; IPR001580; Calreticulin.
DR InterPro; IPR000886; ER_target.
DR Pfam; PF00262; calreticulin; 1.
DR PRINTS; PR00626; CALRETICULIN.
DR PRODOM; PD001866; Calreticulin; 1.
DR PROSITE; PS00014; ER_TARGET; 1.
DR PROSITE; PS00803; CALRETICULIN_1; 1.
DR PROSITE; PS00804; CALRETICULIN_2; 1.
DR PROSITE; PS00805; CALRETICULIN_REPEAT; 2.
KW Endoplasmic reticulum; Calcium-binding; Repeat; Signal; Glycoprotein.
FT SIGNAL 1 22 POTENTIAL.
FT CHAIN 23 421 CALRETICULIN.
FT CARBOHYD 56 56 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 156 156 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT SITE 418 421 PREVENT SECRETION FROM ER (POTENTIAL).
SQ SEQUENCE 421 AA; 48416 MW; 4F5F94CBA6C6690 CRC64;

Query Match 54.3%; Score 527; DB 1; Length 421;
Best Local Similarity 55.3%; Pred. No. 3.7e-40;
Matches 99; Conservative 28; Mismatches 46; Indels 6; Gaps 3;
```


GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: January 14, 2002, 08:48:49 ; Search time 23.38 Seconds
(without alignments)
570.282 Million cell updates/sec

Title: US-09-828-000-3
 perfect score: 180
 Sequence: 1 EPAPVFKQFLDGDGWTGRW.....PDNTYEVKIDNSOVESGSL 180

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 522463 seqs, 74073290 residues

Word size : 18

Total number of hits satisfying chosen parameters: 14

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database : A_Geneseq_1101:*

1: /SID8/gcgdata/geneseq/geneseqp/AA1980.DAT.*
2: /SID8/gcgdata/geneseq/geneseqp/AA1981.DAT.*
3: /SID8/gcgdata/geneseq/geneseqp/AA1982.DAT.*
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8: /SID8/gcgdata/geneseq/geneseqp/AA1987.DAT.*
9: /SID8/gcgdata/geneseq/geneseqp/AA1988.DAT.*
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20: /SID8/gcgdata/geneseq/geneseqp/AA1999.DAT.*
21: /SID8/gcgdata/geneseq/geneseqp/AA2000.DAT.*
22: /SID8/gcgdata/geneseq/geneseqp/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	180	100.0	180	21	AA92351
2	180	100.0	400	21	AA92350
3	180	100.0	417	10	AA92276
4	180	100.0	417	21	AA92349
5	162	90.0	417	20	AA900927
6	77	42.8	401	18	AAW11156
7	61	33.9	61	21	AA92352
8	60	33.3	60	21	AA92354
9	60	33.3	280	21	AA92355
10	49	27.2	49	21	AA92353
11	36	20.0	122	20	AA900934

ALIGNMENTS

RESULT 1

RECEIVED
AAY92351
ID AAY92351 standard; Protein; 180 AA.

XX

AC AAY92351;

XX

DT	10-AUG-2000 (first entry)
XX	
DE	Human vasostatin (calreticulin N-terminal 180 amino acids).

MW-calreticulin; maltose binding protein; vasostatin; N-terminal;
 angiogenesis; inhibition; endothelial cell; anti-angiogenic;
 neuroprotective; antidiabetic; cytostatic; dermatological; hepatic;
 immunosuppressive; antiinflammatory; anti-atherosclerotic;
 gastrointestinal; anti-arthritis; ophthalmic.

XX
50
OS
Homo sapiens.

OS	Homolog sapie
OS	Synthetic:

OS
XX
PN

X

PD	13-APR-2000.
XX	
PF	05-OCT-1999; 99WO-US23240.

XX
XX

PR 06-OCT-1998; 98US-0103438.
XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX
XXXXX()
XXXXXXXXXXXXXXXXXXXX

PI Tosato G, Pike SE,

X

DR WPI; 2000-303767/26.

XX

PT Inhibiting endothelial cell growth and angiogenesis using calreticulin,

PT useful for suppressing tumor growth

PS Claim 4: Page 82: 99pp: English.

A novel method of inhibiting endothelial cell growth comprises contacting the cells with calreticulin (or its fragments/variants). Fragments of calreticulin causes at least 40% inhibition of angiogenesis and tumor growth and/or endothelial cell growth (claimed). The method used for inhibiting angiogenesis in a patient. The angiogenesis is associated with a disease other than a tumor that is associated with neovascularization (e.g. diabetic neuropathy, retrolental fibroplasia, trachoma, neovascular glaucoma, psoriasis, angiofibromas, immune inflammation, atherosclerosis, excessive wound repair, retinal neovascularization, macular degeneration, corneal graft rejection, contact lens overwear, Crohn's disease, non-immune inflammation, rheumatoid arthritis, systemic lupus erythematosus, thyroiditis, Goodpasture's syndrome, systemic vasculitis, scleroderma, Sjogren's syndrome, sarcoidosis and primary biliary cirrhosis). The method may also be used for treating/inhibiting tumor growth especially Kaposi's sarcoma (claimed).

XX	Sequence	180 AA;
SQ		

Query Match	100.0%;	Score 180;	DB 21;	Length 180;
Best Local Similarity	100.0%;	Pred. No. 2e-187;		

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[illegible]

QY 61 SASFPFNSKGGTLVQFTVKEHQNIDCGGYYKLFPSNSLQDTMHGSEYNIMFGPDIC 120
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 Db 61 sasfepfnskgtllvvqftvkheqndcgggyvklfpnsldqtdmhgdsenymfpgdic 120
 |||||
 QY 121 GPGTKKVHVIFNYKGNKVLINKDIRCKDDEFTHLYTLVRPNTYEVKIDNSQVSGSLE 180
 |||||
 Db 121 gpgtkkvhvifnykgknvlinkdirckddefthlytlvrpntyevevkdnsqvesgsle 180
 |||||
 RESULT 2
 AAY92350
 ID AAY92350 standard; Protein: 400 AA.
 XX
 AC AAY92350;
 XX
 DT 10-AUG-2000 (first entry)
 XX
 DE Recombinant human MBP-calreticulin.
 XX
 KW MBP-calreticulin; maltose binding protein; angiogenesis; inhibition;
 KW endothelial cell; anti-angiogenic; neuroprotective; antidiabetic;
 KW cytostatic; dermatological; immunosuppressive; antiinflammatory; hepatic;
 KW anti-atherosclerotic; gastrointestinal; anti-arthritis; ophthalmic.
 XX
 OS Homo sapiens.
 XX
 PN WO200020577-A1.
 XX
 PD 13-APR-2000.
 XX
 PF 05-OCT-1999; 99WO-US23240.
 XX
 PR 06-OCT-1998; 98US-0103438.
 XX
 PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
 XX
 PI Toesato G, Pike SE, Yao L;
 XX
 DR WPI; 2000-303767/26.
 DR N-PSDB; AAA09346, AAA09347.
 XX
 PT Inhibiting endothelial cell growth and angiogenesis using calreticulin,
 useful for suppressing tumor growth
 XX
 PS Claim 4; Page 80-81; 99pp; English.
 XX
 CC Recombinant human MBP-calreticulin comprises the sequence of human
 calreticulin (see AAY92349) without the 17 N-terminal amino acids.
 CC A novel method of inhibiting endothelial cell growth comprises
 contacting the cells with calreticulin (or its fragments/variants).
 CC Fragments of calreticulin causes at least 40% inhibition of
 angiogenesis, tumor growth and/or endothelial cell growth (claimed). The
 method may be used for inhibiting angiogenesis in a patient. The
 angiogenesis is associated with a disease other than a tumor that is
 associated with neovascularization (e.g. diabetic neuropathy, retrolental
 fibroplasia, trachoma, neovascular glaucoma, psoriasis, angiofibromas,
 immune inflammation, atherosclerosis, excessive wound repair, retinal
 neovascularization, macular degeneration, corneal graft rejection,
 contact lens overwear, Crohn's disease, non-immune inflammation,
 rheumatoid arthritis, systemic lupus erythematosus, thyroiditis,
 Goodpasture's syndrome, systemic vasculitis, scleroderma, Sjorgen's
 syndrome, sarcoidosis and primary biliary cirrhosis). The method may
 also be used for treating/inhibiting tumor growth especially
 Kaposi's sarcoma (claimed).
 XX
 SQ Sequence 400 AA;

Query Match 100.0%; Score 180; DB 21; Length 400;
 Best Local Similarity 100.0%; Pred. No. 4.1e-187;
 Matches 180; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EPAYVFKQFLDGDGWTSRWIESKHKSDFGKFLVSSGKFYGDDEKDKGLQTSQDARFYAL 60
 |||||
 Db 1 epavyfkeqfldgdgwtarwieskhksdfgkflvssgkfygdeekdkgltsqdarfyal 60
 |||||
 QY 61 SASFPFNSKGGTLVQFTVKEHQNIDCGGYYKLFPSNSLQDTMHGSEYNIMFGPDIC 120
 |||||
 Db 61 sasfepfnskgtllvvqftvkheqndcgggyvklfpnsldqtdmhgdsenymfpgdic 120
 |||||
 QY 121 GPGTKKVHVIFNYKGNKVLINKDIRCKDDEFTHLYTLVRPNTYEVKIDNSQVSGSLE 180
 |||||
 Db 121 gpgtkkvhvifnykgknvlinkdirckddefthlytlvrpntyevevkdnsqvesgsle 180
 |||||
 RESULT 3
 AAP92276
 ID AAP92276 standard; protein: 417 AA.
 XX
 AC AAP92276;
 XX
 DT 23-FEB-1990 (first entry)
 XX
 DE 60 kD Ro (Ro/SSA) antigen.
 XX
 KW Sjorens syndrome; systemic lupus erythematosus.
 XX
 OS Synthetic.
 XX
 PN WO8909273-A.
 XX
 PD 05-OCT-1989.
 XX
 PF 22-MAR-1989; 89WO-US01213.
 XX
 PR 22-MAR-1988; 88US-0171634.
 XX
 PA (TEXA) UNIV OF TEXAS SYST.
 XX
 PI Sontheimer RD, Capra JD, McCauliffe DP;
 XX
 DR WPI; 1989-309537/42.
 DR N-PSDB; AAP92276.
 XX
 PT DNA sequences encoding antigenic epitope(s) of Ro 60 kD autoantigen
 - used in immunoassays to detect rheumatic disease
 XX
 PS Disclosure; Fig 2; 88pp; English.
 XX
 CC Synthetic peptides corresp. to an epitopic core of Ro antigen are
 expressed recombinantly to detect autoantibodies, for identification
 of autoimmune diseases. These epitopes are AAs 24-36, 23-36, 188-209,
 or 241-255. The peptides may be substd. for ribonucleoprotein particle
 antigens.
 XX
 SQ Sequence 417 AA;

Query Match 100.0%; Score 180; DB 10; Length 417;
 Best Local Similarity 100.0%; Pred. No. 4.2e-187;
 Matches 180; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EPAYVFKQFLDGDGWTSRWIESKHKSDFGKFLVSSGKFYGDDEKDKGLQTSQDARFYAL 60
 |||||
 Db 18 epavyfkeqfldgdgwtarwieskhksdfgkflvssgkfygdeekdkgltsqdarfyal 77
 |||||
 QY 61 SASFPFNSKGGTLVQFTVKEHQNIDCGGYYKLFPSNSLQDTMHGSEYNIMFGPDIC 120
 |||||
 Db 78 sasfepfnskgtllvvqftvkheqndcgggyvklfpnsldqtdmhgdsenymfpgdic 137
 |||||
 QY 121 GPGTKKVHVIFNYKGNKVLINKDIRCKDDEFTHLYTLVRPNTYEVKIDNSQVSGSLE 180
 |||||
 Db 138 gpgtkkvhvifnykgknvlinkdirckddefthlytlvrpntyevevkdnsqvesgsle 197
 |||||

RESULT 4
 AAY92349
 ID AAY92349 standard; Protein; 417 AA.
 XX
 AC AAY92349;
 XX
 DT 10-AUG-2000 (first entry)
 XX
 DE Human MBP-calreticulin.
 XX
 KW MBP-calreticulin; maltose binding protein; angiogenesis; inhibition;
 KW endothelial cell; anti-angiogenic; neuroprotective; antidiabetic;
 KW cytostatic; dermalogical; immunosuppressive; antiinflammatory; hepatic;
 KW anti-atherosclerotic; gastrointestinal; anti-arthritis; ophthalmic.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Peptide 1..17
 FT /label= signal_peptide
 FT 18
 FT Protein /label= mature_protein
 FT
 FT
 FT
 XX WO200020577-A1.
 XX
 PN
 PD 13-APR-2000.
 XX
 XX 05-OCT-1999; 99WO-US23240.
 XX
 PF
 PR 06-OCT-1998; 98US-0103438.
 XX
 XX (USSH) US DEPT HEALTH & HUMAN SERVICES.
 PA
 XX Tosato G, Pike SE, Yao L;
 PI
 PI WPI: 2000-303767/26.
 XX
 DR N-PSDB; AAA09346, AAA09347.
 XX
 XX Inhibiting endothelial cell growth and angiogenesis using calreticulin,
 PT useful for suppressing tumor growth
 PT
 XX Disclosure; Page 79-80; 99pp; English.
 XX
 PS A novel method of inhibiting endothelial cell growth comprises
 CC contacting the cells with calreticulin (or its fragments/variants).
 CC Fragments of calreticulin causes at least 40% inhibition of angiogenesis,
 CC tumor growth and/or endothelial cell growth (claimed). The method may be
 CC used for inhibiting angiogenesis in a patient. The angiogenesis is
 CC associated with a disease other than a tumor that is associated with
 CC neovascularization (e.g. diabetic neuropathy, retrolental fibroplasia,
 CC trachoma, neovascular glaucoma, psoriasis, angiofibromas, immune
 CC inflammation, atherosclerosis, excessive wound repair, retinal
 CC neovascularization, macular degeneration, corneal graft rejection,
 CC contact lens overwear, Crohn's disease, non-immune inflammation,
 CC rheumatoid arthritis, systemic lupus erythematosus, thyroiditis,
 CC Goodpasture's syndrome, systemic vasculitis, scleroderma, Sjorgen's
 CC syndrome, sarcoidosis and primary biliary cirrhosis). The method may
 CC also be used for treating/inhibiting tumor growth especially
 CC Kaposi's sarcoma (claimed).
 CC
 XX
 SQ Sequence 417 AA;
 Query Match 100.0%; Score 180; DB 21; Length 417;
 Best Local Similarity 100.0%; Pred. No. 4.2e-187;
 Matches 180; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 EPAYYKEQFLDGDGWTSRWIESKHSDFGKVLSSGRFYGDDEKDKGLQTSQDARFYAL 60
 Db 18 epavyfkeqfldgdgwtswieskhsdfgkvlssgkfygdeekdkglqtsqdarfyal 77
 QY 61 SASFEPFSNKGQTLVVQFTVKHEQNIDCGGGYVKLFPNSLDQTMHGDSSEYNIMFGPDIC 120
 Db 18 epavyfkeqfldgdgwtswieskhsdfgkvlssgkfygdeekdkglqtsqdarfyal 77
 QY 61 SASFEPFSNKGQTLVVQFTVKHEQNIDCGGGYVKLFPNSLDQTMHGDSSEYNIMFGPDIC 120
 Db 18 epavyfkeqfldgdgwtswieskhsdfgkvlssgkfygdeekdkglqtsqdarfyal 77

QY 139 LINKTRCKDDETHLYTLIVRPDNTYEVKIDNSQVSGSLE 180
 |||||
 Db 156 linkdirckddefthlytlivrpdpntyevekidnsqvesgsl 179

RESULT 6

AAW11156
 ID AAW11156 standard; peptide; 401 AA.
 XX
 AC AAW11156;
 XX
 DT 31-MAY-1997 (first entry)
 XX
 DE Calreticulin.
 XX
 KW calreticulin; C-domain; restenosis; inhibitor.
 XX
 OS Homo sapiens.
 XX
 PN WO9636643-A1.
 XX
 PD 21-NOV-1996.
 XX
 PF 17-MAY-1996; 96WO-IB00471.
 XX
 PR 16-MAY-1996; 96US-0649417.
 PR 17-MAY-1995; 95US-0442844.
 XX
 PA (UYAL-) UNIV ALBERTA.
 XX
 PI Lucas A, Michalak M;
 XX
 DR WPI; 1997-012036/01.
 XX
 PT Inhibition of restenosis in patients - using calreticulin or a
 PT C-domain polypeptide of calreticulin or a variant with the same
 PT activity.
 XX
 PS Disclosure; Fig 1; 48pp; English.
 XX
 CC The present sequence is calreticulin. It and a C-domain derived peptide
 CC (AAW06736) are useful for treating a patient to inhibit restenosis. The
 CC calreticulin-type cpds. are administered either parenterally,
 CC intravenously or via a catheter and can target areas of vascular damage
 CC to inhibit or prevent restenosis.
 XX
 SQ Sequence 401 AA;

Query Match 42.8%; Score 77; DB 18; Length 401;
 Best Local Similarity 100.0%; Pred. No. 3.1e-75;
 Matches 77; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 104 DMHGDEYNIMFGPDICGGTCKKHVIFNYKGNVLINKDIRCKDDEFTHLYTLIVRPDN 163
 |||||
 Db 104 dmhgdeynimfpgdicgpgtkkhvifnykgnvlinkdirckddefthlytlivrpdn 163
 |||||
 QY 164 TYEVKIDNSQVSGSLE 180
 |||||
 Db 164 tyevkidnsqvesgsl 180
 |||||

RESULT 7

AAAY92352
 ID AAY92352 standard; Protein; 61 AA.
 XX
 AC AAY92352;
 XX
 DT 10-AUG-2000 (first entry)
 XX
 DE Recombinant human calreticulin residues 120-180.
 DE
 KW MBP-calreticulin; maltose binding protein; angiogenesis; inhibition;

KW endothelial cell; anti-angiogenic; neuroprotective; antidiabetic;
 KW cytostatic; dermatologic; immunosuppressive; antiinflammatory; hepatic;
 KW anti-atherosclerotic; gastrointestinal; anti-arthritis; ophthalmic.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 PN WO200020577-A1.
 XX
 PD 13-APR-2000.
 XX
 PF 05-OCT-1999; 99WO-US23240.
 XX
 PR 06-OCT-1998; 98US-0103438.
 XX
 PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
 XX
 PI Tosato G, Pike SE, Yao L;
 XX
 DR WPI; 2000-303767/26.
 XX
 PT Inhibiting endothelial cell growth and angiogenesis using calreticulin,
 PT useful for suppressing tumor growth
 XX
 PS Claim 4; Page 82-83; 99pp; English.
 XX
 CC A novel method of inhibiting endothelial cell growth comprises
 CC contacting the cells with calreticulin (or its fragments/variants).
 CC Fragments of calreticulin causes at least 40% inhibition of angiogenesis,
 CC tumor growth and/or endothelial cell growth (claimed). The method may be
 CC used for inhibiting angiogenesis in a patient. The angiogenesis is
 CC associated with a disease other than a tumor that is associated with
 CC neovascularization (e.g. diabetic neuropathy, retrolental fibroplasia,
 CC trachoma, neovascular glaucoma, psoriasis, angiodermas, immune
 CC inflammation, atherosclerosis, excessive wound repair, retinal
 CC neovascularization, macular degeneration, corneal graft rejection,
 CC contact lens overwear, Crohn's disease, non-immune inflammation,
 CC rheumatoid arthritis, systemic lupus erythematosus, thyroiditis,
 CC Goodpasture's syndrome, systemic vasculitis, scleroderma, Sjorgen's
 CC syndrome, sarcoidosis and primary biliary cirrhosis). The method may
 CC also be used for treating/inhibiting tumor growth especially
 CC Kaposi's sarcoma (claimed).
 XX
 SQ Sequence 61 AA;

Query Match 33.9%; Score 61; DB 21; Length 61;
 Best Local Similarity 100.0%; Pred. No. 1.4e-58;
 Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 120 CGFGTKKHVIFNYKGNVLINKDIRCKDDEFTHLYTLIVRPDNTYEVKIDNSQVSGSL 179
 |||||
 Db 1 cpggtkkhvifnykgnvlinkdirckddefthlytlivrpdpntyevekidnsqvesgsl 60
 |||||
 QY 180 E 180
 |||||
 Db 61 e 61
 |||||

RESULT 8

AAAY92354
 ID AAY92354 standard; Protein; 60 AA.
 XX
 AC AAY92354;
 XX
 DT 10-AUG-2000 (first entry)
 XX
 DE Recombinant human calreticulin residues 121-180.
 XX
 KW MBP-calreticulin; maltose binding protein; angiogenesis; inhibition;
 KW endothelial cell; anti-angiogenic; neuroprotective; antidiabetic;
 KW cytostatic; dermatologic; immunosuppressive; antiinflammatory; hepatic;
 KW anti-atherosclerotic; gastrointestinal; anti-arthritis; ophthalmic.

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XX OS Homo sapiens.
XX OS Synthetic.
XX PN WO200020577-A1.
XX PN 13-APR-2000.
XX XX
XX PF 05-OCT-1999; 99WO-US23240.
XX XX
XX PR 06-OCT-1998; 98US-0103438.
XX PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX PI Tosato G, Pike SE, Yao L;
XX XX
XX DR WPI; 2000-303767/26.
XX XX
XX PT Inhibiting endothelial cell growth and angiogenesis using calreticulin,
XX PT useful for suppressing tumor growth
XX PS Claim 4; Page 85; 99pp; English.
XX XX
XX CC A novel method of inhibiting endothelial cell growth comprises
XX CC contacting the cells with calreticulin (or its fragments/variants).
XX CC Fragments of calreticulin causes at least 40% inhibition of angiogenesis,
XX CC tumor growth and/or endothelial cell growth (claimed). The method may be
XX CC used for inhibiting angiogenesis in a patient. The angiogenesis is
XX CC associated with a disease other than a tumor that is associated with
XX CC neovascularization (e.g. diabetic neuropathy, retrolental fibroplasia,
XX CC trachoma, neovascular glaucoma, psoriasis, angiofibromas, immune
XX CC inflammation, atherosclerosis, excessive wound repair, retinal
XX CC neovascularization, macular degeneration, corneal graft rejection,
XX CC contact lens overwear, Crohn's disease, non-immune inflammation,
XX CC rheumatoid arthritis, systemic lupus erythromatosus, thyroiditis,
XX CC Goodpasture's syndrome, systemic vasculitis, scleroderma, Sjorgen's
XX CC syndrome, sarcoidosis and primary biliary cirrhosis). The method may
XX CC also be used for treating/inhibiting tumor growth especially
XX CC Kaposi's sarcoma (claimed).
XX SQ Sequence 60 AA;

Query Match 33.3%; Score 60; DB 21; Length 60;
Best Local Similarity 100.0%; Pred. No. 1.6e-57;
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 121 GPGTKKHVIFNYKGNVLINKDIRCKDDEFTHLYTLIVRPDNTYEVKIDNSQVSGSLE 180
DB 1 gpgtkkhvifnykgnvlinkdirckddefthlytlivrpndtyevkldnsqvsge 60

RESULT 9
AAY92355
ID AAY92355 standard; Protein; 280 AA.
XX AC AAY92355;
XX XX
XX DT 10-AUG-2000 (first entry)
XX DE Recombinant delta-120 calreticulin.
XX KW MBP-calreticulin; maltose binding protein; angiogenesis; inhibition;
XX KW endothelial cell; anti-angiogenic; neuroprotective; antidiabetic;
XX KW cytosolic; dermalogical; immunosuppressive; antiinflammatory; hepatic;
XX KW anti-atherosclerotic; gastrointestinal; anti-arthritis; ophthalmic.
XX OS Homo sapiens.
XX OS Synthetic.
XX PN WO200020577-A1.
XX PD 13-APR-2000.

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XX PF 05-OCT-1999; 99WO-US23240.
XX PR 06-OCT-1998; 98US-0103438.
XX PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX PI Tosato G, Pike SE, Yao L;
XX XX
XX DR WPI; 2000-303767/26.
XX XX
XX PT Inhibiting endothelial cell growth and angiogenesis using calreticulin,
XX PT useful for suppressing tumor growth
XX PS Claim 4; Page 86; 99pp; English.
XX XX
XX CC This sequence comprises recombinant human calreticulin (AAY92355)
XX CC missing the N-terminal 120 amino acids.
XX CC A novel method of inhibiting endothelial cell growth comprises
XX CC contacting the cells with calreticulin (or its fragments/variants).
XX CC Fragments of calreticulin causes at least 40% inhibition of
XX CC angiogenesis, tumor growth and/or endothelial cell growth (claimed). The
XX CC method may be used for inhibiting angiogenesis in a patient. The
XX CC angiogenesis is associated with a disease other than a tumor that is
XX CC associated with neovascularization (e.g. diabetic neuropathy, retrolental
XX CC fibroplasia, trachoma, neovascular glaucoma, psoriasis, angiofibromas,
XX CC immune inflammation, atherosclerosis, excessive wound repair, retinal
XX CC neovascularization, macular degeneration, corneal graft rejection,
XX CC contact lens overwear, Crohn's disease, non-immune inflammation,
XX CC rheumatoid arthritis, systemic lupus erythromatosus, thyroiditis,
XX CC Goodpasture's syndrome, systemic vasculitis, scleroderma, Sjorgen's
XX CC syndrome, sarcoidosis and primary biliary cirrhosis). The method may
XX CC also be used for treating/inhibiting tumor growth especially
XX CC Kaposi's sarcoma (claimed).
XX SQ Sequence 280 AA;

Query Match 33.3%; Score 60; DB 21; Length 280;
Best Local Similarity 100.0%; Pred. No. 6.5e-57;
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 121 GPGTKKHVIFNYKGNVLINKDIRCKDDEFTHLYTLIVRPDNTYEVKIDNSQVSGSLE 180
DB 1 gpgtkkhvifnykgnvlinkdirckddefthlytlivrpndtyevkldnsqvsge 60

RESULT 10
AAY92353
ID AAY92353 standard; Protein; 49 AA.
XX AC AAY92353;
XX XX
XX DT 10-AUG-2000 (first entry)
XX DE Recombinant human calreticulin residues 132-180.
XX KW MBP-calreticulin; maltose binding protein; angiogenesis; inhibition;
XX KW endothelial cell; anti-angiogenic; neuroprotective; antidiabetic;
XX KW cytosolic; dermalogical; immunosuppressive; antiinflammatory; hepatic;
XX KW anti-atherosclerotic; gastrointestinal; anti-arthritis; ophthalmic.
XX OS Homo sapiens.
XX OS Synthetic.
XX PN WO200020577-A1.
XX PD 13-APR-2000.
XX PF 05-OCT-1999; 99WO-US23240.
XX PR 06-OCT-1998; 98US-0103438.
XX XX

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PA (USSH) US DEPT HEALTH & HUMAN SERVICES.

PI Tosato G, Pike SE, Yao L;

XX WPI; 2000-303767/26.

XX Inhibiting endothelial cell growth and angiogenesis using calreticulin,
PT useful for suppressing tumor growth

XX Claim 4; Page 82-83; 99pp; English.

XX A novel method of inhibiting endothelial cell growth comprises
CC contacting the cells with calreticulin (or its fragments/variants).
CC Fragments of calreticulin causes at least 40% inhibition of angiogenesis,
CC tumor growth and/or endothelial cell growth (claimed). The method may be
CC used for inhibiting angiogenesis in a patient. The angiogenesis is
CC associated with a disease other than a tumor that is associated with
CC neovascularization (e.g. diabetic neuropathy, retrolental fibroplasia,
CC trachoma, neovascular glaucoma, psoriasis, angiofibromas, immune
CC inflammation, atherosclerosis, excessive wound repair, retinal
CC neovascularization, macular degeneration, corneal graft rejection,
CC contact lens overwear, Crohn's disease, non-immune inflammation,
CC rheumatoid arthritis, systemic lupus erythematosus, thyroiditis,
CC Goodpasture's syndrome, systemic vasculitis, scleroderma, Sjorgen's
CC syndrome, sarcoidosis and primary biliary cirrhosis). The method may
CC also be used for treating/inhibiting tumor growth especially
CC Kaposi's sarcoma (claimed).

XX Sequence 49 AA;

Query Match 27.2%; Score 49; DB 21; Length 49;

Best Local Similarity 100.0%; Pred. No. 1.2e-45;

Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 132 NYKGNVLINKDICKDEFTHLYTLVRPDNTYEVKIDNSQVSGSLE 180

Db 1 nykgknvlndickddefthlytlvrpdntyevkldnsqvsgele 49

RESULT 11

AAV00924

ID AAY00924 standard; Protein; 122 AA.

XX AAY00924;

DT 28-MAY-1999 (first entry)

DE Human cClqR binding domain protein sequence.

XX Clq and collectin receptor; cClqR binding domain; complement ubiquitin;
KW CUB functionality; inhibitor; complement activation; inflammation;
KW myocardial infarction; brain ischaemia; gut ischaemia; amyloid plaque;
KW rheumatoid arthritis; systemic lupus erythematosus; Alzheimer's disease;
KW immune complex nephritis; therapy.

OS Homo sapiens.

XX WO9907406-A1.

XX 18-FEB-1999.

XX 12-AUG-1998; 98WO-GB02430.

XX 12-AUG-1997; 97GB-0016998.

XX (UYLE-) UNIV LEICESTER.

XX Schwaeble W;

XX WPI; 1999-180404/15.

XX N-PSDB; AAX27251.

XX

PT Use of a cClqR binding domain - to modulate complement ubiquitin
(CUB) functionality.

XX Claim 9; Page 23; 31pp; English.

XX This sequence is a Clq and collectin receptor (cClqR) binding
CC domain. The invention relates to the use of a cClqR binding domain in a
CC medicament to effect complement ubiquitin (CUB) functionality, and an
CC inhibitor of the cClqR binding domain in a medicament to inhibit CUB
CC functionality. The cClqR binding domain, or its inhibitor, can be used to
CC treat a human or animal body. Particularly an inhibitor is used to treat
CC complement activation involved in the initiation and maintenance of
CC inflammation, for example in myocardial infarction, brain ischaemia
CC (stroke), gut ischaemia, rheumatoid arthritis, systemic lupus
CC erythematosus, burns, immune complex nephritis, and to treat amyloid
CC plaques in Alzheimer's disease. The use of cClqR binding domain or
CC inhibitor enables the CUB domain functionality to be modulated using a
CC low molecular weight molecule.

XX Sequence 122 AA;

Query Match 20.0%; Score 36; DB 20; Length 122;

Best Local Similarity 100.0%; Pred. No. 3.6e-31;

Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 145 RCKDDEFTHLYTLVRPDNTYEVKIDNSQVSGSLE 180

Db 1 rckddefthlytlvrpdntyevkldnsqvsgele 36

RESULT 12

AAV00926

ID AAY00926 standard; Protein; 122 AA.

XX AAY00926;

DT 28-MAY-1999 (first entry)

DE Rat cClqR binding domain protein sequence.

XX Clq and collectin receptor; cClqR binding domain; complement ubiquitin;
KW CUB functionality; inhibitor; complement activation; inflammation;
KW myocardial infarction; brain ischaemia; gut ischaemia; amyloid plaque;
KW rheumatoid arthritis; systemic lupus erythematosus; Alzheimer's disease;
KW immune complex nephritis; therapy.

OS Rattus norvegicus.

XX WO9907406-A1.

XX 18-FEB-1999.

XX 12-AUG-1998; 98WO-GB02430.

XX 12-AUG-1997; 97GB-0016998.

XX (UYLE-) UNIV LEICESTER.

XX Schwaeble W;

XX WPI; 1999-180404/15.

XX N-PSDB; AAX27253.

XX Use of a cClqR binding domain - to modulate complement ubiquitin
(CUB) functionality.

XX Claim 9; Page 24-25; 31pp; English.

XX This sequence is a Clq and collectin receptor (cClqR) binding
CC domain. The invention relates to the use of a cClqR binding domain in a
CC medicament to effect complement ubiquitin (CUB) functionality, and an
CC inhibitor of the cClqR binding domain in a medicament to inhibit CUB

CC functionality. The cClqR binding domain, or its inhibitor, can be used to
 CC treat a human or animal body. Particularly an inhibitor is used to treat
 CC complement activation involved in the initiation and maintenance of
 CC inflammation, for example in myocardial infarction, brain ischaemia
 CC (stroke), gut ischaemia, rheumatoid arthritis, systemic lupus
 CC erythematosus, burns, immune complex nephritis, and to treat amyloid
 CC plaques in Alzheimer's disease. The use of cClqR binding domain or
 CC inhibitor enables the CUB domain functionality to be modulated using a
 CC low molecular weight molecule.
 XX
 SQ Sequence 122 AA;

Query Match 20.0%; Score 36; DB 20; Length 122;
 Best Local Similarity 100.0%; Pred. No. 3.6e-31;
 Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 145 RCKDDETHLYTLIVRPDNTYEVKIDNSQVESGSLE 180
 |||||
 Db 1 rckddefthlytlivrpndtyevkidnsqvesgsle 36

RESULT 13
 AAY00925
 ID AAY00925 standard; Protein; 122 AA.
 XX AC AAY00925;
 XX AC
 XX 28-MAY-1999 (first entry)
 XX DE Mouse cClqR binding domain protein sequence.
 XX Clq and collectin receptor; cClqR binding domain; complement ubiquitin;
 KW CUB functionality; inhibitor; complement activation; inflammation;
 KW myocardial infarction; brain ischaemia; gut ischaemia; amyloid plaque;
 KW rheumatoid arthritis; systemic lupus erythematosus; Alzheimer's disease;
 KW immune complex nephritis; therapy.
 XX OS Mus musculus.
 XX WO9907406-A1.
 XX PN
 XX 18-FEB-1999.
 XX PD
 XX PF 12-AUG-1998; 98WO-GB02430.
 XX PR 12-AUG-1997; 97GB-0016998.
 XX PA (UYLE-) UNIV LEICESTER.
 XX PI
 XX Schwaible W;
 XX WPI: 1999-180404/15.
 XX DR N-PSDB; AAX27252.
 XX PT Use of a cClqR binding domain - to modulate complement ubiquitin
 XX (CUB) functionality.
 XX PS Claim 9; Page 24; 31pp; English.

CC This sequence is a Clq and collectin receptor (cClqR) binding
 CC domain. The invention relates to the use of a cClqR binding domain in a
 CC medicament to effect complement ubiquitin (CUB) functionality, and an
 CC inhibitor of the cClqR binding domain in a medicament to inhibit CUB
 CC functionality. The cClqR binding domain, or its inhibitor, can be used to
 CC treat a human or animal body. Particularly an inhibitor is used to treat
 CC complement activation involved in the initiation and maintenance of
 CC inflammation, for example in myocardial infarction, brain ischaemia
 CC (stroke), gut ischaemia, rheumatoid arthritis, systemic lupus
 CC erythematosus, burns, immune complex nephritis, and to treat amyloid
 CC plaques in Alzheimer's disease. The use of cClqR binding domain or
 CC inhibitor enables the CUB domain functionality to be modulated using a
 CC low molecular weight molecule.

XX SQ Sequence 122 AA;
 Query Match 10.6%; Score 19; DB 20; Length 122;
 Best Local Similarity 100.0%; Pred. No. 1.1e-12;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 162 DNTYEVKIDNSQVESGSLE 180
 |||||
 Db 18 dntyevkidnsqvesgsle 36
 RESULT 14
 AAR12312
 ID AAR12312 standard; Protein; 336 AA.
 XX AC AAR12312;
 XX DT 29-AUG-1991 (first entry)
 XX DE Partial sequence of Onchocera volvulus 42 kD antigen.
 XX KW River blindness; onchocerciasis; vaccine; antigen; parasite.
 XX OS Onchocerca volvulus.
 XX FH Key Location/Qualifiers
 FT Region 160..166
 FT /label= repeat unit
 FT /note= "hydrophilic"
 FT Region 177..183
 FT /label= repeat unit
 FT /note= "hydrophilic"
 FT Region 195..201
 FT /label= repeat unit
 FT /note= "hydrophilic"
 XX US5021342-A.
 XX PN
 XX 04-JUN-1991.
 XX PD
 XX PF 30-JUN-1988; 88US-0214264.
 XX PR 30-JUN-1988; 88US-0214264.
 XX PA (UYHO-) UNIV HOSPITALS CLEV.
 XX PI
 XX Greene BM, Unnasch TR;
 XX WPI: 1991-185179/25.
 XX DR N-PSDB; AAQ11987.
 XX PT DNA encoding Onchocerca volvulus antigen - used to express
 XX recombinant antigen for vaccine against onchocerciasis or river
 XX blindness.
 XX PS Disclosure; Fig 7; 20pp; English.
 XX CC The sequence was deduced from a cDNA clone lambda RAL-1 prep'd.
 CC from RNA isolated from nodules excised from patients infected
 CC with O. volvulus. The N-terminal is incomplete, however Abs
 CC which specifically bind to protein prep'd. from induced cultures
 CC of lambda RAL-1 lysogens recognise a single polypeptide of mol.
 CC wt. 42,000 in extracts of adult worms. Analysis deduced sequence
 CC suggests that it encodes a protein of mol. wt. 39,130. If the
 CC antigen is not subject to post-translational processing this
 CC suggests that most of the coding sequence is present. The three
 CC repeats are highly hydrophilic regions likely to be exposed on
 CC the surface of the antigen and highly immunogenic. Recombinant
 CC antigen expressed by the clone can be used stimulate T-cells of
 CC individuals infected by the parasite to proliferate and may be
 CC used as the basis for a vaccine against Onchocerciasis or river

CC blindness.

XX

SQ Sequence 336 AA;

Query Match 10.6%; Score 19; DB 12; Length 336;

Best Local Similarity 100.0%; Pred. No. 2.6e-12;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 113 IMFGPDICGGTKKVVHVF 131

|||||

Db 76 imfgpdicgpgtkkvhvf 94

Search completed: January 14, 2002, 08:50:53

Job time: 124 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: January 9, 2002, 15:01:12 ; Search time 83.2 Seconds
(without alignments)
24.038 Million cell updates/sec

Title: US-09-828-000-5

Perfect score: 151

Sequence: 1 CGPGTKKHVFYFNKGNVLINKDIRC 27

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 522463 seqs, 74073290 residues

Total number of hits satisfying chosen parameters: 522463

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	151	100.0	61	21	AA192352
2	151	100.0	180	21	AA192351
3	151	100.0	400	21	AA192350
4	151	100.0	401	18	AA111156
5	151	100.0	417	10	AA192276
6	151	100.0	417	20	AA190927
7	151	100.0	417	21	AA192349
8	142	94.0	60	21	AA192354
9	142	94.0	280	21	AA192355
10	139	92.1	403	17	AA1904171
11	121	80.1	336	12	AA192312
					Recombinant human
					Human vasostatin (
					Recombinant human
					Calreticulin. Hom
					60 kD Ro (Ro/SSA)
					Calreticulin. Hom
					Human MBP-calretic
					Recombinant human
					Recombinant delta-
					Flea calreticulin
					Partial sequence o

12	82	54.3	49	21	AA192353	Recombinant human
13	82	54.3	415	22	AAB66341	Castor bean calret
14	82	54.3	415	22	AAB66343	Castor bean calret
15	79	52.3	312	21	AAG24609	Arabidopsis thalia
16	79	52.3	312	21	AAG47933	Arabidopsis thalia
17	79	52.3	332	21	AAG30998	Arabidopsis thalia
18	79	52.3	421	21	AAG4608	Arabidopsis thalia
19	79	52.3	421	21	AAG47932	Arabidopsis thalia
20	79	52.3	424	21	AAG24607	Arabidopsis thalia
21	79	52.3	424	21	AAG47931	Arabidopsis thalia
22	79	52.3	441	21	AAG30997	Arabidopsis thalia
23	79	52.3	444	21	AAG30996	Arabidopsis thalia
24	61	40.4	385	21	AAB32385	Human secreted pro
25	54	35.8	284	21	AA191727	Streptococcus pneu
26	54	35.8	720	22	AA192032	Recombinant P. fur
27	54	35.8	720	22	AA192033	P. furiosus helica
28	51	33.8	848	21	AA198565	Human NCAM 140kD i
29	50	33.1	490	21	AA194742	Arabidopsis thalia
30	49	32.5	9	19	AA1976265	Human calreticulin
31	49	32.5	593	13	AA1928349	Bacillus caldotena
32	49	32.5	876	14	AA1945155	B. stearothermophil
33	49	32.5	876	18	AA1935905	Bacillus stearothe
34	49	32.5	877	13	AA1928348	Bacillus caldotena
35	49	32.5	877	18	AA192845	Bacillus caldotena
36	49	32.5	877	18	AA192846	Bacillus caldotena
37	49	32.5	877	18	AA192847	Bacillus caldotena
38	48	31.8	17	20	AA191879	Peptide Seq ID No:
39	48	31.8	17	20	AA1909101	Cell adhesion reco
40	48	31.8	17	21	AA1978215	N-CAM heparin bind
41	48	31.8	17	21	AA194629	Cell adhesion reco
42	47.5	31.5	213	22	AA190122	C glutamicum prote
43	47	31.1	490	17	AA197733	Arabidopsis adenyl
44	47	31.1	490	17	AA192614	Arabidopsis adenyl
45	47	31.1	490	20	AA199454	Arabidopsis adenyl

ALIGNMENTS

RESULT 1

AA192352

ID AA192352 standard; Protein; 61 AA.

XX

AC AA192352;

XX

DT 10-AUG-2000 (first entry)

XX

DE Recombinant human calreticulin residues 120-180.

XX

MBP-calreticulin; maltose binding protein; angiogenesis; inhibition;

endothelial cell; anti-angiogenic; neuroprotective; antidiabetic;

cytostatic; dermatological; immunosuppressive; antiinflammatory; hepatic;

anti-atherosclerotic; gastrointestinal; anti-arthritis; ophthalmic.

OS Homo sapiens.

OS Synthetic.

XX

PN WO200020577-A1.

XX

PD 13-APR-2000.

XX

PF 05-OCT-1999; 99WO-US23240.

XX

PR 06-OCT-1998; 98US-0103438.

XX

PA (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX

PI Tosato G, Pike SE, Yao L;

XX

DR WPI; 2000-303767/26.

XX

PT Inhibiting endothelial cell growth and angiogenesis using calreticulin,

useful for suppressing tumor growth

XX Claim 4; Page 82-83; 99pp; English.
 PS
 CC A novel method of inhibiting endothelial cell growth comprises
 CC contacting the cells with calreticulin (or its fragments/variants).
 CC Fragments of calreticulin causes at least 40% inhibition of angiogenesis,
 CC tumor growth and/or endothelial cell growth (claimed). The method may be
 CC used for inhibiting angiogenesis in a patient. The angiogenesis is
 CC associated with a disease other than a tumor that is associated with
 CC neovascularization (e.g. diabetic neuropathy, retrolental fibroplasia,
 CC trachoma, neovascular glaucoma, psoriasis, angiofibromas, immune
 CC inflammation, atherosclerosis, excessive wound repair, retinal
 CC neovascularization, macular degeneration, corneal graft rejection,
 CC contact lens overwear, Crohn's disease, non-immune inflammation,
 CC rheumatoid arthritis, systemic lupus erythematosus, thyroiditis,
 CC Goodpasture's syndrome, systemic vasculitis, scleroderma, Sjorgen's
 CC syndrome, sarcoidosis and primary biliary cirrhosis). The method may
 CC also be used for treating/inhibiting tumor growth especially
 CC Kaposi's sarcoma (claimed).
 XX
 SQ Sequence 61 AA;

Query Match 100.0%; Score 151; DB 21; Length 61;
 Best Local Similarity 100.0%; Pred. No. 2.5e-16;
 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGPGTKKHVHIFNYKGNVLINKDIRC 27
 |||||
 Db 1 cpgptkhhvifnykgnvlinkdirc 27

RESULT 2
 AAY92351
 ID AAY92351 standard; Protein; 180 AA.

XX AAY92351;
 XX 10-AUG-2000 (first entry)
 XX Human vasostatin (calreticulin N-terminal 180 amino acids).
 DE
 XX MBP-calreticulin; maltose binding protein; vasostatin; N-terminal;
 KW angiogenesis; inhibition; endothelial cell; anti-angiogenic;
 KW neuroprotective; antidiabetic; cytostatic; dermatological; hepatic;
 KW immunosuppressive; anti-inflammatory; anti-atherosclerotic;
 KW gastrointestinal; anti-arthritis; ophthalmic.

OS Homo sapiens.
 OS Synthetic.
 XX WO2000020577-A1.
 XX 13-APR-2000.
 XX 05-OCT-1999; 99WO-US23240.
 XX 06-OCT-1998; 98US-0103438.
 XX (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX Tosato G, Pike SE, Yao L;
 XX WPI; 2000-303767/26.
 DR Inhibiting endothelial cell growth and angiogenesis using calreticulin,
 XX useful for suppressing tumor growth
 XX Claim 4; Page 82; 99pp; English.

XX A novel method of inhibiting endothelial cell growth comprises
 CC contacting the cells with calreticulin (or its fragments/variants).
 CC Fragments of calreticulin causes at least 40% inhibition of angiogenesis,
 CC tumor growth and/or endothelial cell growth (claimed). The method may be
 CC used for inhibiting angiogenesis in a patient. The angiogenesis is
 CC associated with a disease other than a tumor that is associated with
 CC neovascularization (e.g. diabetic neuropathy, retrolental fibroplasia,
 CC trachoma, neovascular glaucoma, psoriasis, angiofibromas, immune
 CC inflammation, atherosclerosis, excessive wound repair, retinal
 CC neovascularization, macular degeneration, corneal graft rejection,
 CC contact lens overwear, Crohn's disease, non-immune inflammation,
 CC rheumatoid arthritis, systemic lupus erythematosus, thyroiditis,
 CC Goodpasture's syndrome, systemic vasculitis, scleroderma, Sjorgen's
 CC syndrome, sarcoidosis and primary biliary cirrhosis). The method may
 CC also be used for treating/inhibiting tumor growth especially
 CC Kaposi's sarcoma (claimed).
 XX
 SQ Sequence 61 AA;

CC tumor growth and/or endothelial cell growth (claimed). The method may be
 CC used for inhibiting angiogenesis in a patient. The angiogenesis is
 CC associated with a disease other than a tumor that is associated with
 CC neovascularization (e.g. diabetic neuropathy, retrolental fibroplasia,
 CC trachoma, neovascular glaucoma, psoriasis, angiofibromas, immune
 CC inflammation, atherosclerosis, excessive wound repair, retinal
 CC neovascularization, macular degeneration, corneal graft rejection,
 CC contact lens overwear, Crohn's disease, non-immune inflammation,
 CC rheumatoid arthritis, systemic lupus erythematosus, thyroiditis,
 CC Goodpasture's syndrome, systemic vasculitis, scleroderma, Sjorgen's
 CC syndrome, sarcoidosis and primary biliary cirrhosis). The method may
 CC also be used for treating/inhibiting tumor growth especially
 CC Kaposi's sarcoma (claimed).
 XX
 SQ Sequence 180 AA;

Query Match 100.0%; Score 151; DB 21; Length 180;
 Best Local Similarity 100.0%; Pred. No. 9e-16;
 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGPGTKKHVHIFNYKGNVLINKDIRC 27
 |||||
 Db 120 cpgptkhhvifnykgnvlinkdirc 146

RESULT 3
 AAY92350
 ID AAY92350 standard; Protein; 400 AA.

XX AAY92350;
 XX 10-AUG-2000 (first entry)
 XX Recombinant human MBP-calreticulin.
 DE
 XX MBP-calreticulin; maltose binding protein; angiogenesis; inhibition;
 KW endothelial cell; anti-angiogenic; neuroprotective; antidiabetic;
 KW cytostatic; dermatological; immunosuppressive; anti-inflammatory; hepatic;
 KW anti-atherosclerotic; gastrointestinal; anti-arthritis; ophthalmic.
 XX Homo sapiens.
 OS WO2000020577-A1.
 XX 13-APR-2000.
 XX 05-OCT-1999; 99WO-US23240.
 XX 06-OCT-1998; 98US-0103438.
 XX (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX Tosato G, Pike SE, Yao L;
 XX WPI; 2000-303767/26.
 DR N-PSDB; AAA09346, AAA09347.
 XX Inhibiting endothelial cell growth and angiogenesis using calreticulin,
 XX useful for suppressing tumor growth
 XX Claim 4; Page 80-81; 99pp; English.

XX Recombinant human MBP-calreticulin comprises the sequence of human
 CC calreticulin (see AAY92349) without the 17 N-terminal amino acids.
 CC A novel method of inhibiting endothelial cell growth comprises
 CC contacting the cells with calreticulin (or its fragments/variants).
 CC Fragments of calreticulin causes at least 40% inhibition of
 CC angiogenesis, tumor growth and/or endothelial cell growth (claimed). The
 CC method may be used for inhibiting angiogenesis in a patient. The
 CC angiogenesis is associated with a disease other than a tumor that is
 CC associated with neovascularization (e.g. diabetic neuropathy, retrolental
 CC fibroplasia, trachoma, neovascular glaucoma, psoriasis, angiofibromas,
 CC inflammation, atherosclerosis, excessive wound repair, retinal
 CC neovascularization, macular degeneration, corneal graft rejection,
 CC contact lens overwear, Crohn's disease, non-immune inflammation,
 CC rheumatoid arthritis, systemic lupus erythematosus, thyroiditis,
 CC Goodpasture's syndrome, systemic vasculitis, scleroderma, Sjorgen's
 CC syndrome, sarcoidosis and primary biliary cirrhosis). The method may
 CC also be used for treating/inhibiting tumor growth especially
 CC Kaposi's sarcoma (claimed).
 XX
 SQ Sequence 180 AA;

PD 18-FEB-1999.
 XX
 PF 12-AUG-1998; 98WO-GB02430.
 XX
 PR 12-AUG-1997; 97CB-0016998.
 XX
 PA (UYLE-) UNIV LEICESTER.
 XX
 PI Schwaeble W;
 XX
 DR WPI; 1999-180404/15.
 XX
 PT Use of a cClqR binding domain - to modulate complement ubiquitin
 PT (CUB) functionality.
 XX
 PR Disclosure; Page 26-27; 31pp; English.
 XX
 CC This sequence is calreticulin, a homologue of Clq and collectin receptor
 CC (cClqR). The invention relates to the use of a cClqR binding domain in a
 CC medicament to effect complement ubiquitin (CUB) functionality, and an
 CC inhibitor of the cClqR binding domain in a medicament to inhibit CUB
 CC functionality. The cClqR binding domain, or its inhibitor, can be used to
 CC treat a human or animal body. Particularly an inhibitor is used to treat
 CC complement activation involved in the initiation and maintenance of
 CC inflammation, for example in myocardial infarction, brain ischaemia
 CC (stroke), gut ischaemia, rheumatoid arthritis, systemic lupus
 CC erythematosus, burns, immune complex nephritis, and to treat amyloid
 CC plaques in Alzheimer's disease. The use of cClqR binding domain or
 CC inhibitor enables the CUB domain functionality to be modulated using a
 CC low molecular weight molecule.
 XX
 SQ Sequence 417 AA;

Query Match 100.0%; Score 151; DB 20; Length 417;
 Best Local Similarity 100.0%; Pred. No. 2.4e-15;
 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CGPGTKKHVHFIENYKGNVLINKDIRC 27
 DB 137 CGPGTKKHVHFIENYKGNVLINKDIRC 163

RESULT 7
 AAY92349
 ID AAY92349 standard; Protein; 417 AA.
 XX
 AC AAY92349;
 XX
 DT 10-AUG-2000 (first entry)
 XX
 DE Human MBP-calreticulin.
 XX
 KW MBP-calreticulin; maltose binding protein; angiogenesis; inhibition;
 KW endothelial cell; anti-angiogenic; neuroprotective; antidiabetic;
 KW cytostatic; dermatological; immunosuppressive; antiinflammatory; hepatic;
 KW anti-atherosclerotic; gastrointestinal; anti-arthritis; ophthalmic.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Peptide 1..17
 FT /label.. signal_peptide
 FT Protein 18
 FT /label.. mature_protein
 XX
 PN WO200020577-A1.
 XX
 PD 13-APR-2000.
 XX
 PP 05-OCT-1999; 99WO-US23240.
 XX
 PR 06-OCT-1998; 98US-0103438.

XX
 PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
 XX
 PI Tosato G, Pike SE, Yao L;
 XX
 DR WPI; 2000-303767/26.
 XX
 DR N-PSDB; AAA09346, AAA09347.
 XX
 PT Inhibiting endothelial cell growth and angiogenesis using calreticulin,
 PT useful for suppressing tumor growth
 XX
 PS Disclosure; Page 79-80; 99pp; English.
 XX
 CC A novel method of inhibiting endothelial cell growth comprises
 CC contacting the cells with calreticulin (or its fragments/variants).
 CC Fragments of calreticulin causes at least 40% inhibition of angiogenesis,
 CC tumor growth and/or endothelial cell growth (claimed). The method may be
 CC used for inhibiting angiogenesis in a patient. The angiogenesis is
 CC associated with a disease other than a tumor that is associated with
 CC neovascularization (e.g. diabetic neuropathy, retrolental fibroplasia,
 CC trachoma, neovascular glaucoma, psoriasis, angiofibromas, immune
 CC inflammation, atherosclerosis, excessive wound repair, retinal
 CC neovascularization, macular degeneration, corneal graft rejection,
 CC contact lens overwear, Crohn's disease, non-immune inflammation,
 CC rheumatoid arthritis, systemic lupus erythematosus, thyroiditis,
 CC Goodpasture's syndrome, systemic vasculitis, scleroderma, Sjorgen's
 CC syndrome, sarcoidosis and primary biliary cirrhosis). The method may
 CC also be used for treating/inhibiting tumor growth especially
 CC Kaposi's sarcoma (claimed).
 XX
 SQ Sequence 417 AA;

Query Match 100.0%; Score 151; DB 21; Length 417;
 Best Local Similarity 100.0%; Pred. No. 2.4e-15;
 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CGPGTKKHVHFIENYKGNVLINKDIRC 27
 DB 137 CGPGTKKHVHFIENYKGNVLINKDIRC 163

RESULT 8
 AAY92354
 ID AAY92354 standard; Protein; 60 AA.
 XX
 AC AAY92354;
 XX
 DT 10-AUG-2000 (first entry)
 XX
 DE Recombinant human calreticulin residues 121-180.
 XX
 KW MBP-calreticulin; maltose binding protein; angiogenesis; inhibition;
 KW endothelial cell; anti-angiogenic; neuroprotective; antidiabetic;
 KW cytostatic; dermatological; immunosuppressive; antiinflammatory; hepatic;
 KW anti-atherosclerotic; gastrointestinal; anti-arthritis; ophthalmic.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 PN WO200020577-A1.
 XX
 PD 13-APR-2000.
 XX
 PF 05-OCT-1999; 99WO-US23240.
 XX
 PR 06-OCT-1998; 98US-0103438.
 XX
 PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
 XX
 PI Tosato G, Pike SE, Yao L;
 XX
 DR WPI; 2000-303767/26.

The sequence was deduced from a cDNA clone lambda RAL-1 prep'd. from RNA isolated from nodules excised from patients infected with *O. volvulus*. The N-terminal is incomplete, however Abs which specifically bind to protein prep'd. from induced cultures of lambda RAL-1 lysogens recognise a single polypeptide of mol. wt. 42,000 in extracts of adult worms. Analysis deduced sequence suggests that it encodes a protein of mol. wt. 39,130. If the antigen is not subject to post-translational processing this suggests that most of the coding sequence is present. The three

A novel method of inhibiting endothelial cell growth comprises contacting the cells with calreticulin (or its fragments/variants). Fragments of calreticulin causes at least 40% inhibition of angiogenesis, tumor growth and/or endothelial cell growth (claimed). The method may be used for inhibiting angiogenesis in a patient. The angiogenesis is associated with a disease other than a tumor that is associated with neovascularization (e.g. diabetic neuropathy, retrolental fibroplasia, trachoma, neovascular glaucoma, psoriasis, angiofibromas, immune inflammation, atherosclerosis, excessive wound repair, retinal neovascularization, macular degeneration, corneal graft rejection, contact lens overwear, Crohn's disease, non-immune inflammation, rheumatoid arthritis, systemic lupus erythematosus, thyroiditis, Goodpasture's syndrome, systemic vasculitis, scleroderma, Sjorgen's syndrome, sarcoidosis and primary biliary cirrhosis). The method may also be used for treating/inhibiting tumor growth especially Kaposi's sarcoma (claimed).

SQ Sequence 49 AA;

Query Match 54.3%; Score 82; DB 21; Length 49;
Best Local Similarity 100.0%; Pred. No. 1.2e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 NYKGNVLINKDIRC 27
|||||
Db 1 nykgknvlinkdirc 15

RESULT 13

AAB66341
ID AAB66341 standard; Protein: 415 AA.

AC AAB66341;

DT 05-APR-2001 (first entry)

XX Castor bean calreticulin SEQ ID NO: 2.

DE Castor bean; calreticulin; calcium binding; er; endoplasmic reticulum;
KW calnexin; promoter; resistance.

XX Ricinus communis.

OS US6171864-B1.

PN 09-JAN-2001.

PF 05-JUL-1996; 96US-0675816.

PR 05-JUL-1996; 96US-0675816.

XX (PTON-) PIONEER HI-BRED INT INC.

PI Coughlan SJ, Winfrey RJ;

DR WPI; 2001-122335/13.

DR N-PSDB; AAF29741, AAF29742.

XX New nucleic acid molecules encoding a calcium binding chaperone protein
in endoplasmic reticulum, calreticulin, and calreticulin promoter
sequences, useful for producing foreign gene products in plant cells

PS Claim 1; Fig 3; 45pp; English.

XX The present invention provides the protein and coding sequences for the
castor bean calreticulin protein and the calreticulin promoter sequence.
CC In addition, the castor bean calnexin protein, coding sequence and
promoter are also described. Calreticulin and calnexin are calcium
binding proteins found in the endoplasmic reticulum (er). The
calreticulin promoter sequence can be used in vectors to promote the
expression of foreign genes, particularly resistance genes, in plant
cells.

SQ Sequence 415 AA;

Query Match 54.3%; Score 82; DB 22; Length 415;
Best Local Similarity 55.6%; Pred. No. 0.00015;
Matches 15; Conservative 2; Mismatches 10; Indels 0; Gaps 0;

QY 1 CGPGTKKHVIFNYKGNVLINKDIRC 27
||| ||||| ||| ||| |||
Db 138 cgystkvhailnyndtnhlikkevpc 164

RESULT 14

AAB66343
ID AAB66343 standard; Protein: 415 AA.

XX

AC AAB66343;

DT 05-APR-2001 (first entry)

DE Castor bean calreticulin.

XX Castor bean; calreticulin; calcium binding; er; endoplasmic reticulum;
KW calnexin; promoter; resistance.

XX Ricinus communis.

PN US6171864-B1.

PD 09-JAN-2001.

PF 05-JUL-1996; 96US-0675816.

PR 05-JUL-1996; 96US-0675816.

XX (PTON-) PIONEER HI-BRED INT INC.

PI Coughlan SJ, Winfrey RJ;

DR WPI; 2001-122335/13.

DR N-PSDB; AAF29755.

XX New nucleic acid molecules encoding a calcium binding chaperone protein
in endoplasmic reticulum, calreticulin, and calreticulin promoter
sequences, useful for producing foreign gene products in plant cells

PS Disclosure; Fig 1B; 45pp; English.

XX The present invention provides the protein and coding sequences for the
castor bean calreticulin protein and the calreticulin promoter sequence.
CC In addition, the castor bean calnexin protein, coding sequence and
promoter are also described. Calreticulin and calnexin are calcium
binding proteins found in the endoplasmic reticulum (er). The
calreticulin promoter sequence can be used in vectors to promote the
expression of foreign genes, particularly resistance genes, in plant
cells.

SQ Sequence 415 AA;

Query Match 54.3%; Score 82; DB 22; Length 415;
Best Local Similarity 55.6%; Pred. No. 0.00015;
Matches 15; Conservative 2; Mismatches 10; Indels 0; Gaps 0;

QY 1 CGPGTKKHVIFNYKGNVLINKDIRC 27
||| ||||| ||| ||| |||
Db 138 cgystkvhailnyndtnhlikkevpc 164

RESULT 15

AAG24609

ID AAG24609 standard; Protein: 312 AA.

AC AAG24609;

DT 17-OCT-2000 (first entry)

DE Arabidopsis thaliana protein fragment SEQ ID NO: 28351.

XX Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
termination sequence.

XX Arabidopsis thaliana.

OS Arabidopsis thaliana.

PN EP1033405-A2.

XX 06-SEP-2000.

PF 25-FEB-2000; 2000EP-0301439.
XX 25-FEB-1999; 99US-0121825.
PR 05-MAR-1999; 99US-0123180.
PR 09-MAR-1999; 99US-0123548.
PR 23-MAR-1999; 99US-0125788.
PR 25-MAR-1999; 99US-0126264.
PR 29-MAR-1999; 99US-0126785.
PR 01-APR-1999; 99US-0127462.
PR 06-APR-1999; 99US-0128234.
PR 08-APR-1999; 99US-0128714.
PR 16-APR-1999; 99US-0129845.
PR 19-APR-1999; 99US-0130077.
PR 21-APR-1999; 99US-0130449.
PR 23-APR-1999; 99US-0130510.
PR 23-APR-1999; 99US-0130891.
PR 28-APR-1999; 99US-0131449.
PR 30-APR-1999; 99US-0132048.
PR 30-APR-1999; 99US-0132407.
PR 04-MAY-1999; 99US-0132484.
PR 05-MAY-1999; 99US-0132485.
PR 06-MAY-1999; 99US-0132486.
PR 06-MAY-1999; 99US-0132487.
PR 07-MAY-1999; 99US-0132863.
PR 11-MAY-1999; 99US-0134256.
PR 14-MAY-1999; 99US-0134218.
PR 14-MAY-1999; 99US-0134219.
PR 14-MAY-1999; 99US-0134221.
PR 14-MAY-1999; 99US-0134370.
PR 18-MAY-1999; 99US-0134768.
PR 19-MAY-1999; 99US-0134941.
PR 20-MAY-1999; 99US-0135124.
PR 21-MAY-1999; 99US-0135353.
PR 24-MAY-1999; 99US-0135629.
PR 25-MAY-1999; 99US-0136021.
PR 27-MAY-1999; 99US-0136392.
PR 28-MAY-1999; 99US-0136782.
PR 01-JUN-1999; 99US-0137222.
PR 03-JUN-1999; 99US-0137528.
PR 04-JUN-1999; 99US-0137502.
PR 07-JUN-1999; 99US-0137724.
PR 08-JUN-1999; 99US-0138094.
PR 10-JUN-1999; 99US-0138540.
PR 10-JUN-1999; 99US-0138847.
PR 14-JUN-1999; 99US-0139119.
PR 16-JUN-1999; 99US-0139452.
PR 16-JUN-1999; 99US-0139453.
PR 17-JUN-1999; 99US-0139492.
PR 18-JUN-1999; 99US-0139454.
PR 18-JUN-1999; 99US-0139455.
PR 18-JUN-1999; 99US-0139456.
PR 18-JUN-1999; 99US-0139457.
PR 18-JUN-1999; 99US-0139458.
PR 18-JUN-1999; 99US-0139459.
PR 18-JUN-1999; 99US-0139460.
PR 18-JUN-1999; 99US-0139461.
PR 18-JUN-1999; 99US-0139462.
PR 18-JUN-1999; 99US-0139463.
PR 18-JUN-1999; 99US-0139750.
PR 18-JUN-1999; 99US-0139763.
PR 21-JUN-1999; 99US-0139817.
PR 22-JUN-1999; 99US-0139899.
PR 23-JUN-1999; 99US-0140353.
PR 23-JUN-1999; 99US-0140354.
PR 24-JUN-1999; 99US-0140695.
PR 28-JUN-1999; 99US-0140823.
PR 29-JUN-1999; 99US-0140991.
PR 30-JUN-1999; 99US-0141287.
PR 01-JUL-1999; 99US-0141842.
PR 01-JUL-1999; 99US-0142154.
PR 02-JUL-1999; 99US-0142058.
PR 06-JUL-1999; 99US-0142390.
PR 08-JUL-1999; 99US-0142803.
PR 09-JUL-1999; 99US-0142920.
PR 12-JUL-1999; 99US-0142977.
PR 13-JUL-1999; 99US-0143542.
PR 14-JUL-1999; 99US-0143624.
PR 15-JUL-1999; 99US-0144005.
PR 16-JUL-1999; 99US-0144085.
PR 16-JUL-1999; 99US-0144086.
PR 19-JUL-1999; 99US-0144325.
PR 19-JUL-1999; 99US-0144331.
PR 19-JUL-1999; 99US-0144332.
PR 19-JUL-1999; 99US-0144333.
PR 19-JUL-1999; 99US-0144334.
PR 19-JUL-1999; 99US-0144335.
PR 20-JUL-1999; 99US-0144352.
PR 20-JUL-1999; 99US-0144632.
PR 20-JUL-1999; 99US-0144684.
PR 21-JUL-1999; 99US-0144814.
PR 21-JUL-1999; 99US-0145086.
PR 21-JUL-1999; 99US-0145088.
PR 22-JUL-1999; 99US-0145085.
PR 22-JUL-1999; 99US-0145087.
PR 22-JUL-1999; 99US-0145089.
PR 22-JUL-1999; 99US-0145192.
PR 23-JUL-1999; 99US-0145145.
PR 23-JUL-1999; 99US-0145218.
PR 23-JUL-1999; 99US-0145224.
PR 26-JUL-1999; 99US-0145276.
PR 27-JUL-1999; 99US-0145913.
PR 27-JUL-1999; 99US-0145918.
PR 27-JUL-1999; 99US-0145919.
PR 28-JUL-1999; 99US-0145951.
PR 02-AUG-1999; 99US-0146386.
PR 02-AUG-1999; 99US-0146388.
PR 03-AUG-1999; 99US-0146389.
PR 04-AUG-1999; 99US-0147038.
PR 04-AUG-1999; 99US-0147204.
PR 05-AUG-1999; 99US-0147302.
PR 05-AUG-1999; 99US-0147192.
PR 06-AUG-1999; 99US-0147260.
PR 06-AUG-1999; 99US-0147303.
PR 09-AUG-1999; 99US-0147493.
PR 09-AUG-1999; 99US-0147935.
PR 10-AUG-1999; 99US-0148171.
PR 11-AUG-1999; 99US-0148319.
PR 12-AUG-1999; 99US-0148341.
PR 13-AUG-1999; 99US-0148565.
PR 13-AUG-1999; 99US-0148684.
PR 16-AUG-1999; 99US-0149368.
PR 17-AUG-1999; 99US-0149175.
PR 18-AUG-1999; 99US-0149426.
PR 20-AUG-1999; 99US-0149722.
PR 20-AUG-1999; 99US-0149723.
PR 20-AUG-1999; 99US-0149922.
PR 23-AUG-1999; 99US-0149902.
PR 23-AUG-1999; 99US-0149930.
PR 25-AUG-1999; 99US-0150566.
PR 26-AUG-1999; 99US-0150884.
PR 27-AUG-1999; 99US-0151065.
PR 27-AUG-1999; 99US-0151066.
PR 27-AUG-1999; 99US-0151080.
PR 30-AUG-1999; 99US-0151303.
PR 31-AUG-1999; 99US-0151438.
PR 01-SEP-1999; 99US-0151930.
PR 07-SEP-1999; 99US-0152363.
PR 10-SEP-1999; 99US-0153070.
PR 13-SEP-1999; 99US-0153758.
PR 15-SEP-1999; 99US-0154018.
PR 16-SEP-1999; 99US-0154039.
PR 20-SEP-1999; 99US-0154779.
PR 22-SEP-1999; 99US-0155139.
PR 23-SEP-1999; 99US-0155486.
PR 24-SEP-1999; 99US-0155659.

PR 28-SEP-1999; 99US-0156458.
PR 29-SEP-1999; 99US-0156596.
PR 04-OCT-1999; 99US-0157117.
PR 05-OCT-1999; 99US-0157753.
PR 06-OCT-1999; 99US-0157865.
PR 07-OCT-1999; 99US-0158029.
PR 08-OCT-1999; 99US-0158232.
PR 12-OCT-1999; 99US-0158369.
PR 13-OCT-1999; 99US-0159293.
PR 13-OCT-1999; 99US-0159294.
PR 13-OCT-1999; 99US-0159295.
PR 14-OCT-1999; 99US-0159329.
PR 14-OCT-1999; 99US-0159330.
PR 14-OCT-1999; 99US-0159331.
PR 14-OCT-1999; 99US-0159637.
PR 14-OCT-1999; 99US-0159638.
PR 18-OCT-1999; 99US-0159584.
PR 21-OCT-1999; 99US-0160741.
PR 21-OCT-1999; 99US-0160767.
PR 21-OCT-1999; 99US-0160768.
PR 21-OCT-1999; 99US-0160770.
PR 21-OCT-1999; 99US-0160814.
PR 21-OCT-1999; 99US-0160815.
PR 22-OCT-1999; 99US-0160980.
PR 22-OCT-1999; 99US-0160981.
PR 22-OCT-1999; 99US-0160989.
PR 25-OCT-1999; 99US-0161404.
PR 25-OCT-1999; 99US-0161405.
PR 25-OCT-1999; 99US-0161406.
PR 26-OCT-1999; 99US-0161359.
PR 26-OCT-1999; 99US-0161360.
PR 26-OCT-1999; 99US-0161361.
PR 28-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161992.
PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

Query Match 52.3%; Score 79; DB 21; Length 312;
Best Local Similarity 55.6%; Pred. NO. 0.00032;
Matches 15; Conservative 1; Mismatches 11; Indels 0; Gaps 0;

OY 1 CGPGTKKHVHVIENYKGNVLINKDIRC 27
Db 28 cgystkvhallityneanhlikkdvpc 54

Search completed: January 9, 2002, 15:01:13
Job time: 159 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: January 9, 2002, 14:58:34 ; Search time 83.2 Seconds
(without alignments)
160.255 Million cell updates/sec

Title: US-09-828-000-3
Perfect score: 971
Sequence: 1 EFAVYKEQFLDGGWTSRW.....PDNTYEVKIDNSOVESGSL 180

Scoring table:
BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 522463 seqs, 74073290 residues

Total number of hits satisfying chosen parameters: 522463

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_1101.*
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22: /SID88/gcgdata/geneseq/geneseq/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query	Score	Match	Length	ID	Description
1	971	100.0	180	21	AA92351	Human vasostatin (
2	971	100.0	400	21	AA92350	Recombinant human
3	971	100.0	417	21	AA92276	60 kD Ro (Ro/SSA)
4	971	100.0	417	21	AA92349	Human MBP-calretic
5	966	99.5	417	20	AA900927	Calreticulin. Hom
6	921	94.9	401	18	AAW11156	Calreticulin. Hom
7	700	72.1	403	17	AAW04171	Flea calreticulin
8	631	65.0	385	21	AA92385	Human secreted pro
9	541.5	55.8	336	12	AA92312	Partial sequence o
10	527	54.3	415	22	AAB66341	Castor bean calret
11	527	54.3	415	22	AAB66343	Castor bean calret

12	510	52.5	421	21	AAG24608	Arabidopsis thalia
13	510	52.5	421	21	AAG47932	Arabidopsis thalia
14	510	52.5	424	21	AAG24607	Arabidopsis thalia
15	510	52.5	424	21	AAG47931	Arabidopsis thalia
16	510	52.5	441	21	AAG30997	Arabidopsis thalia
17	510	52.5	444	21	AAG30996	Arabidopsis thalia
18	327	33.7	61	21	AA92352	Recombinant human
19	318	32.7	60	21	AA92354	Recombinant human
20	318	32.7	280	21	AA92355	Recombinant delta-
21	301.5	31.1	417	21	AA977953	A. thaliana enviro
22	290	29.9	593	16	AA971094	Calnexin sequence.
23	258	26.6	49	21	AA92353	Recombinant human
24	253	26.1	312	21	AAG24609	Arabidopsis thalia
25	253	26.1	312	21	AAG47933	Arabidopsis thalia
26	253	26.1	332	21	AAG30998	Arabidopsis thalia
27	250.5	25.8	84	21	AAG41018	Zea mays protein f
28	238.5	24.6	530	21	AAG26284	Arabidopsis thalia
29	238.5	24.6	530	21	AAG46611	Arabidopsis thalia
30	238.5	24.6	567	21	AAG46610	Arabidopsis thalia
31	227.5	23.4	542	22	AAB66342	Castor bean calnex
32	200.5	20.6	532	21	AAG04448	Arabidopsis thalia
33	200.5	20.6	548	21	AAG04447	Arabidopsis thalia
34	190	19.6	122	20	AA900924	Human cC1qR bindin
35	190	19.6	122	20	AA900926	Rat cC1qR binding
36	182	18.7	122	20	AA900925	Mouse cC1qR bindin
37	145	14.9	91	21	AAG34014	Arabidopsis thalia
38	145	14.9	99	21	AAG34013	Arabidopsis thalia
39	140.5	14.5	256	22	AAB99168	Human Endoplasmic
40	124.5	12.8	221	21	AAB56468	Human prostate can
41	114.5	11.8	162	21	AAG00147	Human secreted pro
42	114.5	11.8	162	21	AAG00148	Human secreted pro
43	112.5	11.6	394	21	AAG26285	Arabidopsis thalia
44	112.5	11.6	394	21	AAG46612	Arabidopsis thalia
45	110.5	11.4	125	21	AAG25999	Zea mays protein f

ALIGNMENTS

RESULT 1
AA92351
ID AA92351 standard; Protein; 180 AA.
AC AA92351;
XX
XX
DT 10-AUG-2000 (first entry)
XX
DE Human vasostatin (calreticulin N-terminal 180 amino acids).
XX
KW MBP-calreticulin; maltose binding protein; vasostatin; N-terminal;
KW angiogenesis; inhibition; endothelial cell; anti-angiogenic;
KW neuroprotective; antidiabetic; cytostatic; dermatological; hepatic;
KW immunosuppressive; antiinflammatory; anti-atherosclerotic;
KW gastrointestinal; anti-arthritis; ophthalmic.
XX
OS Homo sapiens.
OS Synthetic.
XX
XX
PN WO200020577-A1.
XX
PD 13-APR-2000.
XX
XX
PF 05-OCT-1999; 99WO-US23240.
XX
PR 06-OCT-1998; 98US-0103438.
XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Tosato G, Pike SE, Yao L;
XX
DR WPI; 2000-303767/26.
XX
PT Inhibiting endothelial cell growth and angiogenesis using calreticulin,

PT useful for suppressing tumor growth
 XX Claim 4; Page 82; 99pp; English.
 XX A novel method of inhibiting endothelial cell growth comprises
 CC contacting the cells with calreticulin (or its fragments/variants).
 CC Fragments of calreticulin causes at least 40% inhibition of angiogenesis,
 CC tumor growth and/or endothelial cell growth (claimed). The method may be
 CC used for inhibiting angiogenesis in a patient. The angiogenesis is
 CC associated with a disease other than a tumor that is associated with
 CC neovascularization (e.g. diabetic neuropathy, retrolental fibroplasia,
 CC trachoma, neovascular glaucoma, psoriasis, angiofibromas, immune
 CC inflammation, atherosclerosis, excessive wound repair, retinal
 CC neovascularization, macular degeneration, corneal graft rejection,
 CC contact lens overwear, Crohn's disease, non-immune inflammation,
 CC rheumatoid arthritis, systemic lupus erythematosus, thyroiditis,
 CC Goodpasture's syndrome, systemic vasculitis, scleroderma, Sjorgen's
 CC syndrome, sarcoidosis and primary biliary cirrhosis). The method may
 CC also be used for treating/inhibiting tumor growth especially
 CC Kaposi's sarcoma (claimed).
 XX Sequence 180 AA;

Query Match 100.0%; Score 971; DB 21; Length 180;
 Best Local Similarity 100.0%; Pred. No. 3.1e-95;
 Matchew 180; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 PPAVYFKQFLDGDGWTSRWIESKHKSDPGKFLVSSGKFGYGDDEKDKGLQTSQDARFYAL 60
 DB 1 PPAVYFKQFLDGDGWTSRWIESKHKSDPGKFLVSSGKFGYGDDEKDKGLQTSQDARFYAL 60
 QY 61 SASPEPFSNKGOTLVVQFTVKEQNDICGGYVVKLFPSNLSQDTMHGDSSEYNIMFGPDIC 120
 DB 61 SASPEPFSNKGOTLVVQFTVKEQNDICGGYVVKLFPSNLSQDTMHGDSSEYNIMFGPDIC 120
 QY 121 GPQTKKVVHIFNYKGNKVLINKDIRCKDDEFTHLYTLVRPNTVEVKIDNSQVSGSLE 180
 DB 121 GPQTKKVVHIFNYKGNKVLINKDIRCKDDEFTHLYTLVRPNTVEVKIDNSQVSGSLE 180

RESULT 2
 AAY92350
 ID AAY92350 standard; Protein; 400 AA.
 AC AAY92350;
 DT 10-AUG-2000 (first entry)
 DE Recombinant human MBP-calreticulin.
 KW MBP-calreticulin; maltose binding protein; angiogenesis; inhibition;
 KW endothelial cell; anti-angiogenic; neuroprotective; antidiabetic;
 KW cytostatic; dermatological; immunosuppressive; anti-inflammatory; hepatic;
 KW anti-atherosclerotic; gastrointestinal; anti-arthritis; ophthalmic.
 OS Homo sapiens.
 XX WO200020577-A1.
 PN 13-APR-2000.
 PD 05-OCT-1999; 99WO-US23240.
 PF 06-OCT-1999; 98US-0103438.
 XX (USSH) US DEPT HEALTH & HUMAN SERVICES.
 PA Tosato G, Pike SE, Yao L;
 PI WPI: 2000-303767/26.
 DR N-PSDB; AAA09346, AAA09347.
 XX

PT Inhibiting endothelial cell growth and angiogenesis using calreticulin,
 XX useful for suppressing tumor growth
 XX Claim 4; Page 80-81; 99pp; English.
 XX Recombinant human MBP-calreticulin comprises the sequence of human
 CC calreticulin (see AAY92349) without the 17 N-terminal amino acids.
 CC A novel method of inhibiting endothelial cell growth comprises
 CC contacting the cells with calreticulin (or its fragments/variants).
 CC Fragments of calreticulin causes at least 40% inhibition of
 CC angiogenesis, tumor growth and/or endothelial cell growth (claimed). The
 CC method may be used for inhibiting angiogenesis in a patient. The
 CC angiogenesis is associated with a disease other than a tumor that is
 CC associated with neovascularization (e.g. diabetic neuropathy, retrolental
 CC fibroplasia, trachoma, neovascular glaucoma, psoriasis, angiofibromas,
 CC immune inflammation, atherosclerosis, excessive wound repair, retinal
 CC neovascularization, macular degeneration, corneal graft rejection,
 CC contact lens overwear, Crohn's disease, non-immune inflammation,
 CC rheumatoid arthritis, systemic lupus erythematosus, thyroiditis,
 CC Goodpasture's syndrome, systemic vasculitis, scleroderma, Sjorgen's
 CC syndrome, sarcoidosis and primary biliary cirrhosis). The method may
 CC also be used for treating/inhibiting tumor growth especially
 CC Kaposi's sarcoma (claimed).
 XX Sequence 400 AA;

Query Match 100.0%; Score 971; DB 21; Length 400;
 Best Local Similarity 100.0%; Pred. No. 9.4e-99;
 Matches 180; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 PPAVYFKQFLDGDGWTSRWIESKHKSDPGKFLVSSGKFGYGDDEKDKGLQTSQDARFYAL 60
 DB 1 PPAVYFKQFLDGDGWTSRWIESKHKSDPGKFLVSSGKFGYGDDEKDKGLQTSQDARFYAL 60
 QY 61 SASPEPFSNKGOTLVVQFTVKEQNDICGGYVVKLFPSNLSQDTMHGDSSEYNIMFGPDIC 120
 DB 61 SASPEPFSNKGOTLVVQFTVKEQNDICGGYVVKLFPSNLSQDTMHGDSSEYNIMFGPDIC 120
 QY 121 GPQTKKVVHIFNYKGNKVLINKDIRCKDDEFTHLYTLVRPNTVEVKIDNSQVSGSLE 180
 DB 121 GPQTKKVVHIFNYKGNKVLINKDIRCKDDEFTHLYTLVRPNTVEVKIDNSQVSGSLE 180

RESULT 3
 AAP92276
 ID AAP92276 standard; protein; 417 AA.
 XX AAP92276;
 AC AAP92276;
 DT 23-FEB-1990 (first entry)
 DE 60 kD Ro (Ro/SSA) antigen.
 KW Sjorens syndrome; systemic lupus erythematosus.
 OS Synthetic.
 XX WO8909273-A.
 PN 05-OCT-1989.
 PD 22-MAR-1989; 89WO-US01213.
 PF 22-MAR-1989; 88US-0171634.
 XX (TEXA) UNIV OF TEXAS SYST.
 PA Sontheimer RD, Capra JD, McCauliffe DP;
 PI WPI: 1989-309537/42.
 DR N-PSDB; AAP92276.
 XX

PT DNA sequences encoding antigenic epitope(s) of Ro 60 kD autoantigen
 XX - used in immunoassays to detect rheumatic disease
 PS Disclosure; Fig 2; 88pp; English.
 XX
 CC Synthetic peptides corresp. to an epitopic core of Ro antigen are
 CC expressed recombinantly to detect autoantibodies, for identification
 CC of autoimmune diseases. These epitopes are AAs 24-36, 23-36, 188-209,
 CC or 241-255. The peptides may be substd. for ribonucleoprotein particle
 CC antigens.
 XX
 SQ Sequence 417 AA;

Query Match 100.0%; Score 971; DB 10; Length 417;
 Best Local Similarity 100.0%; Pred. No. 9.9e-99;
 Matches 180; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EPAVYFKEQFLDGDGWTSRWIESKHKSDFGKFLVSSGKFGYGDDEKDKGLQTSQDARFYAL 60
 |||||
 DB 18 epavyfkeqfldgdgwtswieskhksdfgkflvssgkfygdeekdkglqtsqdarfyal 77
 |||||

QY 61 SASFPEFSNKGQTLVVOFTVKHEQNIDCGGVYKLFPPNSLDQTMHGDSEYNIMFGPDIC 120
 |||||
 DB 78 sasfepfsnkgqtlvvqftvkheqnidcgggyvklfpnsldqtdmhdgdeynimfpgdic 137
 |||||

QY 121 GPGTKKVHVFYFNKGNVLINKDIRCKDDEFTHLYTLIVRPONTYEVKIDNSQVESGSLE 180
 |||||
 DB 138 gpgtkkvhvfynkgnvlinkdirckddefthlytlivrpontyevkidnsqvesgsle 197
 |||||

RESULT 4
 AAY92349
 ID AAY92349 standard; Protein; 417 AA.
 XX
 AC AAY92349;
 XX
 DT 10-AUG-2000 (first entry)
 XX
 DE Human MBP-calreticulin.
 XX
 KW MBP-calreticulin; maltose binding protein; angiogenesis; inhibition;
 KW endothelial cell; anti-angiogenic; neuroprotective; antidiabetic;
 KW cytosolic; dermatological; immunosuppressive; antiinflammatory; hepatic;
 KW anti-atherosclerotic; gastrointestinal; anti-arthritis; ophthalmic.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Peptide 1..17
 FT /label= signal_peptide
 FT Protein 18
 FT /label= mature_protein
 XX
 PN WO200020577-A1.
 XX
 PD 13-APR-2000.
 XX
 PF 05-OCT-1999; 99WO-US23240.
 XX
 PR 06-OCT-1998; 98US-0103438.
 XX
 PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
 XX
 PI Tosato G, Pike SE, Yao L;
 XX
 DR WPI; 2000-303767/26.
 DR N-PSDB; AAA09346, AAA09347.
 XX
 PT Inhibiting endothelial cell growth and angiogenesis using calreticulin,
 PT useful for suppressing tumor growth
 XX
 PS Disclosure; Page 79-80; 99pp; English.

XX A novel method of inhibiting endothelial cell growth comprises
 CC contacting the cells with calreticulin (or its fragments/variants).
 CC Fragments of calreticulin causes at least 40% inhibition of angiogenesis,
 CC tumor growth and/or endothelial cell growth (claimed). The method may be
 CC used for inhibiting angiogenesis in a patient. The angiogenesis is
 CC associated with a disease other than a tumor that is associated with
 CC neovascularization (e.g. diabetic neuropathy, retrolental fibroplasia,
 CC trachoma, neovascular glaucoma, psoriasis, angiofibromas, immune
 CC inflammation, atherosclerosis, excessive wound repair, retinal
 CC neovascularization, macular degeneration, corneal graft rejection,
 CC contact lens overwear, Crohn's disease, non-immune inflammation,
 CC rheumatoid arthritis, systemic lupus erythromatosus, thyroiditis,
 CC Goodpasture's syndrome, systemic vasculitis, scleroderma, Sjorgen's
 CC syndrome, sarcoidosis and primary biliary cirrhosis). The method may
 CC also be used for treating/inhibiting tumor growth especially
 CC Kaposi's sarcoma (claimed).
 XX
 SQ Sequence 417 AA;

Query Match 100.0%; Score 971; DB 21; Length 417;
 Best Local Similarity 100.0%; Pred. No. 9.9e-99;
 Matches 180; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EPAVYFKEQFLDGDGWTSRWIESKHKSDFGKFLVSSGKFGYGDDEKDKGLQTSQDARFYAL 60
 |||||
 DB 18 epavyfkeqfldgdgwtswieskhksdfgkflvssgkfygdeekdkglqtsqdarfyal 77
 |||||

QY 61 SASFPEFSNKGQTLVVOFTVKHEQNIDCGGVYKLFPPNSLDQTMHGDSEYNIMFGPDIC 120
 |||||
 DB 78 sasfepfsnkgqtlvvqftvkheqnidcgggyvklfpnsldqtdmhdgdeynimfpgdic 137
 |||||

QY 121 GPGTKKVHVFYFNKGNVLINKDIRCKDDEFTHLYTLIVRPONTYEVKIDNSQVESGSLE 180
 |||||
 DB 138 gpgtkkvhvfynkgnvlinkdirckddefthlytlivrpontyevkidnsqvesgsle 197
 |||||

RESULT 5
 AAY00927
 ID AAY00927 standard; Protein; 417 AA.
 XX
 AC AAY00927;
 XX
 DT 28-MAY-1999 (first entry)
 XX
 DE Calreticulin.
 XX
 KW Clq and collectin receptor; cClqR binding domain; complement ubiquitin;
 KW CUB functionality; inhibitor; complement activation; inflammation;
 KW myocardial infarction; brain ischaemia; gut ischaemia; amyloid plaque;
 KW rheumatoid arthritis; systemic lupus erythematosis; Alzheimer's disease;
 KW immune complex nephritis; therapy.
 XX
 OS Homo sapiens.
 XX
 PN WO9907406-A1.
 XX
 PD 18-FEB-1999.
 XX
 PF 12-AUG-1998; 98WO-GB02430.
 XX
 PR 12-AUG-1997; 97GB-0016998.
 XX
 PA (UYLE-) UNIV LEICESTER.
 XX
 PI Schwaeble W;
 XX
 DR WPI; 1999-180404/15.
 XX
 PT Use of a cClqR binding domain - to modulate complement ubiquitin
 PT (CUB) functionality.
 XX


```

SQ Sequence 403 AA;
      Query Match      72.1%; Score 700; DB 17; Length 403;
      Best Local Similarity 71.7%; Pred. No. 7.8e-69;
      Matches 129; Conservative 23; Mismatches 26; Indels 2; Gaps 2;
QY 2 PAVYFKEQFLDGGWTSRWIESKHK-SDFGKFLVSSGKFGYDEERDKGLQTSQDARFYALS 60
DB 19 pefvleefnd-dtwntwysehpgkefgkfvhtagkyfndaeadkglqtggrdaryal 77
QY 61 SASFSPFNKGGOTLVVQFTVKHEQNIDCGGGVVKLPFNSLDQTDHGDSEYNIMFGPDIC 120
DB 78 shkfpfsnkdktlvvqfsvkneqndoggyikgfetsvndkdmngespyeimfgpdic 137
QY 121 GPGTKKVVHIFNYKGNVLINKDIRKODEFTHLYTLIVRPDNTVEVKIDNSQVSGSLE 180
DB 138 dpgtkkvhvifsykgnkvnlinkdirckddvthvylvvpdntyevidnckvesgnle 197
      RESULT 8
      AAB32385
      ID AAB32385 standard; Protein; 385 AA.
      XX
      AC AAB32385;
      XX
      DT 16-JAN-2001 (first entry)
      XX
      DE Human secreted protein sequence encoded by gene 15 SEQ ID NO:71.
      KW Human; secreted protein; cytostatic; immunostimulant; antiproliferative;
      KW cardiant; antiarrhythmic; antiviral; antibacterial; antifungal; cancer;
      KW antiparasitic; neuroprotective; nootropic; antiinflammatory; anti-HIV;
      KW antiangiogenic; antiarteriosclerotic; diagnosis; immune disorder; AIDS;
      KW autoimmune disease; haematopoietic cell disorder; blood protein disorder;
      KW agammaglobulinaemia; hyperproliferative disease; gaucher's disease;
      KW cardiovascular disorder; congenital heart defect; pulmonary atresia;
      KW arrhythmia; ischaemia; angiogenesis related disorder; Crohn's disease;
      KW atherosclerosis; neurological disease; Alzheimer's disease;
      KW Huntington's; infectious disease; cat-scratch disease.
      XX
      OS Homo sapiens.
      XX
      PN WO200047602-A1.
      XX
      PD 17-AUG-2000.
      XX
      PF 08-FEB-2000; 2000WO-US03062.
      XX
      PR 10-FEB-1999; 99US-0119468.
      XX
      PA (HUMA-) HUMAN GENOME SCI INC.
      XX
      PI Rosen CA, Ruben SM, Ebner R, Young PE, Ni J, Soppet DR, Moore PA;
      PI Shi Y, Lafleur DW, Olsen HS, Florence KA, Komatsoulis G;
      XX
      DR WPI: 2000-543578/49.
      DR N-PSDB; AAC55204.
      XX
      PT New human nucleic acids encoding secreted proteins, useful in the
      PT treatment, prevention or diagnosis of immune disorders (e.g. autoimmune
      PT diseases), blood protein disorders and hyperproliferative diseases
      PT (e.g. Gaucher's disease) -
      XX
      PS Claim 11; Page 434-435; 488pp; English.
      XX
      CC The polynucleotide sequences given in AAC55190 to AAC55235 encode the
      CC human secreted proteins given in AAB32371 to AAB32484. Human secreted
      CC proteins have activities based on the tissues and cells the genes are
      CC expressed in. Examples of activities include: cytostatic;
      CC immunostimulant; antiproliferative; cardiant; antiarrhythmic; antiviral;
      CC antibacterial; antifungal; antiparasitic; neuroprotective; nootropic;
      CC antiinflammatory; antiangiogenic; anti-HIV; and antiarteriosclerotic. The

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CC polynucleotides and polypeptides, or their agonists and antagonists, can
CC be used for treating, preventing or diagnosing immune disorders (e.g.
CC cancer, autoimmune diseases), disorders of haematopoietic cells, blood
CC protein disorders (e.g. agammaglobulinaemia), hyperproliferative
CC diseases (e.g. Gaucher's disease), cardiovascular disorders (e.g.
CC congenital heart defects, pulmonary atresia, arrhythmias, ischaemia),
CC angiogenesis related disorders (e.g. Crohn's disease, atherosclerosis),
CC neurological diseases (e.g. Alzheimer's disease, Huntington's chorea),
CC infectious diseases (e.g. AIDS, cat-scratch disease and other bacterial,
CC viral, parasitic or fungal diseases). AAC55181 to AAC55189 and AAB32370
CC represent sequences used in the exemplification of the present
CC invention.
XX
SQ Sequence 385 AA;
      Query Match      65.0%; Score 631; DB 21; Length 385;
      Best Local Similarity 64.4%; Pred. No. 3e-61;
      Matches 114; Conservative 30; Mismatches 33; Indels 0; Gaps 0;
QY 4 VYFKEQFLDGGWTSRWIESKHKSDFGKFLVSSGKFGYDEERDKGLQTSQDARFYALSAS 63
DB 21 vyfgeefldgehwrrwlqstndsrfgfhlssgkfyghkekdkglqtqngrfyaisar 80
QY 64 FEPFNSKGGOTLVVQFTVKHEQNIDCGGGVVKLPFNSLDQTDHGDSEYNIMFGPDICGPG 123
DB 81 fkpfsnkgktlvlyqvtvkheqkmdcgggyikvfpadidgknkngsqyymfpgpdicgd 140
QY 124 TKKKVVHIFNYKGNVLINKDIRKODEFTHLYTLIVRPDNTVEVKIDNSQVSGSLE 180
DB 141 ikkvvhlhfknyhenkklirckvdgftlhylirpalsydvkldgsgsiesg 197
      RESULT 9
      AAR12312
      ID AAR12312 standard; Protein; 336 AA.
      XX
      AC AAR12312;
      XX
      DT 29-AUG-1991 (first entry)
      XX
      DE Partial sequence of Onchocera volvulus 42 kD antigen.
      XX
      KW River blindness; onchocerciasis; vaccine; antigen; parasite.
      XX
      OS Onchocerca volvulus.
      XX
      FH Key Location/Qualifiers
      FT Region 160..166
      FT /label= repeat unit
      FT /note= "hydrophilic"
      FT Region 177..183
      FT /label= repeat unit
      FT /note= "hydrophilic"
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      FT /note= "hydrophilic"
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      PN US021342-A.
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      PD 04-JUN-1991.
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      PF 30-JUN-1988; 88US-0214264.
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      PR 30-JUN-1988; 88US-0214264.
      XX
      PA (UYHO-) UNIV HOSPITALS CLEV.
      XX
      PI Greene BM, Unnasch TR;
      XX
      DR WPI: 1991-185179/25.
      DR N-PSDB; AAQ11987.
      XX

```

PT DNA encoding Onchocerca volvulus antigen - used to express
PT recombinant antigen for vaccine against onchocerciasis or river
PT blindness.

PS Disclosure; Fig 7; 20pp; English.

XX The sequence was deduced from a cDNA clone lambda RAL-1 prep.
CC from RNA isolated from nodules excised from patients infected
CC with O. volvulus. The N-terminal is incomplete, however Abs
CC which specifically bind to protein prep. from induced cultures
CC of lambda RAL-1 lysogens recognise a single polypeptide of mol.
CC wt. 42,000 in extracts of adult worms. Analysis deduced sequence
CC suggests that it encodes a protein of mol. wt. 39,130. If the
CC antigen is not subject to post-translational processing this
CC suggests that most of the coding sequence is present. The three
CC repeats are highly hydrophilic regions likely to be exposed on
CC the surface of the antigen and highly immunogenic. Recombinant
CC antigen expressed by the clone can be used stimulate T-cells of
CC individuals infected by the parasite to proliferate and may be
CC used as the basis for a vaccine against Onchocerciasis or river
CC blindness.

SQ Sequence 336 AA;

Query Match 55.8%; Score 541.5; DB 12; Length 336;
Best Local Similarity 68.5%; Pred. No. 1.9e-51;
Matches 98; Conservative 21; Mismatches 23; Indels 1; Gaps 1;

QY 39 FYGDEEKGLQTSQDARFVALSASPE-PFSNKGQTLVVQFTVKHQNDICGGYVKLFP 97
DB 1 fygdavkdkqklttdaktyisgaktidsfnskgslvqfsvkheqldcggqyvklna 60
QY 48 NSLDQTMHGDSEYNIWFGDPCGCTKKVHVIFNYKGNVLINKDIRCKDDEFTHLYTL 157
DB 61 advnledshqetpyhmfipdpcgptkvvhvifhykdrnmikdkirckddvftlhlytl 120
QY 158 IVRPNTYEVKIDNSQVESGLE 180
DB 121 ivnsdntcyevqidqkaesgele 143

RESULT 10
AAB66341
ID AAB66341 standard; Protein; 415 AA.
AC AAB66341;
XX 05-APR-2001 (first entry)
XX Castor bean calreticulin SEQ ID NO: 2.

XX Castor bean; calreticulin; calcium binding; er; endoplasmic reticulum;
KW calnexin; promoter; resistance.
XX Ricinus communis.
XX US6171864-B1.
XX 09-JAN-2001.
XX 05-JUL-1996; 96US-0675816.
XX 05-JUL-1996; 96US-0675816.
XX (PION-) PIONEER HI-BRED INT INC.
XX Coughlan SJ, Winfrey RJ;
XX WPI; 2001-122335/13.
XX N PSDB; AAF29741, AAF29742.
XX New nucleic acid molecules encoding a calcium binding chaperone protein

PT in endoplasmic reticulum, calreticulin, and calreticulin promoter
PT sequences, useful for producing foreign gene products in plant cells -
XX Claim 1; Fig 3; 45pp; English.

XX The present invention provides the protein and coding sequences for the
CC castor bean calreticulin protein and the calreticulin promoter sequence.
CC In addition, the castor bean calnexin protein, coding sequence and
CC promoter are also described. Calreticulin and calnexin are calcium
CC binding proteins found in the endoplasmic reticulum (er). The
CC calreticulin promoter sequence can be used in vectors to promote the
CC expression of foreign genes, particularly resistance genes, in plant
CC cells.

SQ Sequence 415 AA;

Query Match 54.3%; Score 527; DB 22; Length 415;
Best Local Similarity 55.3%; Pred. No. 1e-49;
Matches 99; Conservative 31; Mismatches 43; Indels 6; Gaps 3;

QY 4 VYFKEQFLDCGWTSRWIESKHKSD---FGKEVLSGKPYGDEEKDKGLQTSQDARFVAL 60
DB 22 vfeeri--edgwenrwksdwdkddentagwnylsgkwnqd-pndkgqltseedyrfyal 78
QY 61 SASFPFSSNKGQTLVVQFTVKHQNDICGGYVKLFPNSLDQTMHGDSEYNIWFGPDIC 120
DB 79 saefpfsnkgkhtlvqfsvkheqldcgggymkllssatdkgkfsgdtpyslmfpgdic 138
QY 121 GPCTKKVHVIFNYKGNVLINKDIRCKDDEFTHLYTLIVRPNTYEVKIDNSQVESGSL 179
DB 139 gystkvvhailnyndtnhlikkevpcetdqlthvylvirpdatysilidnvekqlgs 197

RESULT 11
AAB66343
ID AAB66343 standard; Protein; 415 AA.

XX AAB66343;
XX 05-APR-2001 (first entry)
XX Castor bean calreticulin.
XX Castor bean; calreticulin; calcium binding; er; endoplasmic reticulum;
KW calnexin; promoter; resistance.
XX Ricinus communis.
XX US6171864-B1.
XX 09-JAN-2001.
XX 05-JUL-1996; 96US-0675816.
XX 05-JUL-1996; 96US-0675816.
XX (PION-) PIONEER HI-BRED INT INC.
XX Coughlan SJ, Winfrey RJ;
XX WPI; 2001-122335/13.
XX N PSDB; AAF29755.
XX New nucleic acid molecules encoding a calcium binding chaperone protein
PT in endoplasmic reticulum, calreticulin, and calreticulin promoter
PT sequences, useful for producing foreign gene products in plant cells -
XX Disclosure; Fig 1B; 45pp; English.
XX The present invention provides the protein and coding sequences for the
CC castor bean calreticulin protein and the calreticulin promoter sequence.
CC In addition, the castor bean calnexin protein, coding sequence and

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Best Local Similarity 53.9%; Pred. No. 7.8e-48;

Matches 97; Conservative 30; Mismatches 47; Indels 6; Gaps 3;

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QY 60 LSASFEPFSNKQOTLVVQFTVRHEQNIQDCGGYVKLFPSNLQDTMHGDSYNNIMFGPDI 119

Db 80 isaepefsnkdktlvfqfsvkheqklDCggymkllsgdvqkkggdtptysimfgpdi 139

QY 120 CGPGTKKHVIFNYKGNVLINKDIRCKDDEFTHLVTLVRPDNTYEVKIDNSQVSSGSL 179

Db 140 cgystkvhailtyneanhlikkdvpcetdqlthvytflrpdatsilidnvektqtsl 199

RESULT 15

AAG47931

ID AAG47931 standard; Protein; 424 AA.

XX

AC AAG47931;

XX

DT 18-OCT-2000 (first entry)

XX

DE Arabidopsis thaliana protein fragment SEQ ID NO: 60468.

XX

KW Protein identification; signal transduction pathway; metabolic pathway;

KW hybridisation assay; genetic mapping; gene expression control; promoter;

KW termination sequence.

XX

OS Arabidopsis thaliana.

XX

PN EP1033405-A2.

XX

PD 06-SEP-2000.

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PF 25-FEB-2000; 2000EP-0301439.

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PR 25-FEB-1999; 99US-0121825.

PR 05-MAR-1999; 99US-0123180.

PR 09-MAR-1999; 99US-0123548.

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PR 09-AUG-1999; 99US-0147493.
PR 09-AUG-1999; 99US-0147935.
PR 10-AUG-1999; 99US-0147935.
PR 11-AUG-1999; 99US-0148171.
PR 12-AUG-1999; 99US-0148319.
PR 13-AUG-1999; 99US-0148341.
PR 13-AUG-1999; 99US-0148565.
PR 16-AUG-1999; 99US-0148684.
PR 16-AUG-1999; 99US-0149368.
PR 17-AUG-1999; 99US-0149175.
PR 18-AUG-1999; 99US-0149426.
PR 20-AUG-1999; 99US-0149722.
PR 20-AUG-1999; 99US-0149723.
PR 20-AUG-1999; 99US-0149929.
PR 23-AUG-1999; 99US-0149902.
PR 23-AUG-1999; 99US-0149930.
PR 25-AUG-1999; 99US-0150566.
PR 26-AUG-1999; 99US-0150884.
PR 27-AUG-1999; 99US-0151065.
PR 27-AUG-1999; 99US-0151066.
PR 27-AUG-1999; 99US-0151080.
PR 30-AUG-1999; 99US-0151303.
PR 31-AUG-1999; 99US-0151438.
PR 01-SEP-1999; 99US-0151930.
PR 07-SEP-1999; 99US-0152363.
PR 10-SEP-1999; 99US-0153070.
PR 13-SEP-1999; 99US-0153758.
PR 15-SEP-1999; 99US-0154018.
PR 16-SEP-1999; 99US-0154039.
PR 20-SEP-1999; 99US-0154779.
PR 22-SEP-1999; 99US-0155139.
PR 23-SEP-1999; 99US-0155486.
PR 24-SEP-1999; 99US-0155659.
PR 28-SEP-1999; 99US-0156458.
PR 29-SEP-1999; 99US-0156596.
PR 04-OCT-1999; 99US-0157117.
PR 05-OCT-1999; 99US-0157753.
PR 06-OCT-1999; 99US-0157865.
PR 07-OCT-1999; 99US-0158029.
PR 08-OCT-1999; 99US-0158232.
PR 12-OCT-1999; 99US-0158369.
PR 13-OCT-1999; 99US-0159293.
PR 13-OCT-1999; 99US-0159294.
PR 13-OCT-1999; 99US-0159295.
PR 14-OCT-1999; 99US-0159329.
PR 14-OCT-1999; 99US-0159330.
PR 14-OCT-1999; 99US-0159331.
PR 14-OCT-1999; 99US-0159637.
PR 14-OCT-1999; 99US-0159638.
PR 18-OCT-1999; 99US-0159584.
PR 21-OCT-1999; 99US-0160741.
PR 21-OCT-1999; 99US-0160767.
PR 21-OCT-1999; 99US-0160768.
PR 21-OCT-1999; 99US-0160770.
PR 21-OCT-1999; 99US-0160814.
PR 21-OCT-1999; 99US-0160815.
PR 22-OCT-1999; 99US-0160980.

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: January 9, 2002, 14:58:58 ; Search time 78.15 Seconds
(without alignments)
336.904 Million cell updates/sec

Title: US-09-828-000-3
Perfect score: 971
Sequence: 1 EPAVYFKEQFLDGGWTSRW.....PDNTYEVKIDNSQVESGSL 180

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 473505 seqs, 146272329 residues

Total number of hits satisfying chosen parameters: 473505

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SPTREMBL_17.*

- 1: sp_archaea.*
- 2: sp_bacteria.*
- 3: sp_fungi.*
- 4: sp_human.*
- 5: sp_invertebrate.*
- 6: sp_mammal.*
- 7: sp_mmc.*
- 8: sp_organelle.*
- 9: sp_phage.*
- 10: sp_plant.*
- 11: sp_rodent.*
- 12: sp_virus.*
- 13: sp_invertebrate.*
- 14: sp_unclassified.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	835	86.0	411	13 Q91710	Q91710 xenopus lae
2	804	82.8	405	5 Q26268	Q26268 aplysia cal
3	797	82.1	343	13 Q91711	Q91711 xenopus lae
4	796	82.0	419	13 Q98984	Q98984 rana rugosa
5	785	80.8	417	13 Q9PUC1	Q9pucl brachydanio
6	759	78.2	410	5 Q16893	Q16893 amblyomma a
7	731	75.3	421	5 Q9U6S0	Q9u6s0 strongyloce
8	699	72.0	406	5 Q9U916	Q9u916 drosophila
9	681.5	70.2	403	5 Q76961	Q76961 necator ame
10	680	70.0	387	5 Q97372	Q97372 dirofilaria
11	673	69.3	375	5 Q18478	Q18478 litomosoides
12	641	66.0	380	11 Q9D906	Q9d906 mus musculus
13	539	55.5	412	10 Q40040	Q40040 hordeum vul
14	539	55.5	415	10 Q40041	Q40041 hordeum vul
15	536	55.2	421	10 Q43712	Q43712 zea mays (m
16	514.5	53.2	389	10 Q40567	Q40567 nicotiana t
17	514.5	53.0	427	10 Q9FYV2	Q9fyv2 pinus taeda
18	507.5	52.3	396	5 Q45034	Q45034 schistosoma
19	477.5	49.2	350	5 Q26514	Q26514 schistosoma

20	464.5	47.8	240	10 Q9ST29	Q9st29 solanum mel
21	460	47.4	318	13 Q9PTX7	Q9ptx7 lampetra re
22	450	46.3	214	4 Q9UDG2	Q9udg2 homo sapien
23	448.5	46.2	403	5 Q9XYF8	Q9xyf8 trypanosoma
24	446.5	46.0	401	5 Q9U9N9	Q9u9n9 trypanosoma
25	409.5	42.2	291	5 Q9Y1V1	Q9y1v1 leishmania
26	392	40.4	397	5 Q94592	Q94592 leishmania
27	373	38.4	321	13 Q9U5G0	Q9u5g0 eptatretus
28	347	35.7	422	10 Q22502	Q22502 brassica na
29	329.5	33.9	321	10 Q41799	Q41799 zea mays (m
30	302.5	31.2	101	10 Q40751	Q40751 parthenium
31	289.5	29.8	582	3 Q9HEC6	Q9hec6 varrowia li
32	270	27.8	578	11 Q9D2K5	Q9d2k5 mus musculu
33	264.5	27.2	559	5 Q9NG26	Q9ng26 tritricthomo
34	263.5	27.1	581	5 Q9BLH3	Q9blh3 halocynthia
35	262	27.0	622	13 Q98985	Q98985 rana rugosa
36	251	25.8	70	10 Q9SXW3	Q9sxw3 lithospermu
37	248	25.5	582	5 Q04702	Q04702 schistosoma
38	240	24.7	583	5 Q9VXF6	Q9vxf6 drosophila
39	238.5	24.6	582	5 Q76214	Q76214 schistosoma
40	238.5	24.6	582	5 Q9TVF3	Q9tvf3 schistosoma
41	231.5	23.8	272	4 Q16094	Q16094 homo sapien
42	224	23.1	543	5 Q9VVP4	Q9vvp4 drosophila
43	224	23.1	556	5 Q9I7S9	Q9i7s9 drosophila
44	221.5	22.8	605	5 Q02393	Q02393 drosophila
45	207	21.3	545	5 Q9VAL7	Q9val7 drosophila

ALIGNMENTS

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RESULT 1
Q91710 ID Q91710 PRELIMINARY; PRT; 411 AA.
AC Q91710;
DT 01-JAN-1998 (Tremblrel. 05, Created)
DT 01-JAN-1998 (Tremblrel. 05, Last sequence update)
DE 01-JUN-2001 (Tremblrel. 17, Last annotation update)
DE CALRETICULIN PRECURSOR (FRAGMENT).
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=BRAIN;
RX MEDLINE=93074997; PubMed=1445218;
RA Treves S., Zorzato F., Pozzan T.;
RT "Identification of calreticulin isoforms in the central nervous
   system.";
RL Biochem. J. 287:579-581(1992).
DR EMBL; X67597; CAA47866.1; -.
DR InterPro; IPR000886; ER_target.
DR InterPro; IPR001580; Calreticulin.
DR Pfam; PF00262; calreticulin; 1.
DR PRINTS; PR00626; CALRETICULIN.
DR ProDom; PD001866; Calreticulin; 1.
DR PROSITE; PS00803; CALRETICULIN_1; 1.
DR PROSITE; PS00804; CALRETICULIN_2; 1.
DR PROSITE; PS00805; CALRETICULIN_REPEAT; 2.
DR PROSITE; PS00014; ER_TARGET; UNKNOWN_1.
   Signal.
FT NON_TER 1 12 POTENTIAL.
FT SIGNAL <1 12 CALRETICULIN.
FT CHAIN 13 411
SQ SEQUENCE 411 AA; 48344 MW; 891DA66E0EBEFA CRC64;

```

Query Match 86.0%; Score 835; DB 13; Length 411;
Best Local Similarity 83.9%; Pred. No. 2.7e-71;
Matches 151; Conservative 15; Mismatches 14; Indels 0; Gaps 0;

QY 1 EPAYYFKEQFLDGDGWTSRWIESKHKSDGKFLVSSGKFGYDEKDKGLQTSODARFYAL 60
 DB 13 EPAYYFKEEFTDGDGWTQWRWESKHHTDYGKFLSKAGFYGDSEKDKGLQTSODARFYAM 72
 QY 61 SASFEPFSNKGQTLVQFTVKHQNIDCGGYYKFLPNSLDQTDHMGDSYINMFGPDIC 120
 DB 73 SSREFDSFNKQDQTLVQFVKHQNIDCGGYYKFLPNSLDQTDHMGDSYINMFGPDIC 132
 QY 121 GPOTKKVHVIFNYKGNVLINKIRCKDDDEFTHTLYTLIVRPDNTYEVKIDNSQVESGSLE 180
 DB 133 GPPTKKVHVIFNYKGNVLINKIRCKDDDEFTHTLYTLIVRPDNTYEVKIDNSQVESGSLE 192

RESULT 2
 Q26268 ID Q26268 PRELIMINARY; PRT; 405 AA.
 AC Q26268;
 DT 01-NOV-1996 (Tremblrel. 01, Created)
 DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
 DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)
 DE CALRETICULIN.
 OS Aplysia californica (California sea hare).
 OC Eukaryota; Metazoa; Mollusca; Gastropoda; Opisthobranchia; Anaspidea;
 OC Aplysiidae; Aplysia.
 OX NCBI_TaxID: 6500;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-93098937; PubMed 1463604;
 RA Kennedy T.E., Kuhl D., Barzilai A., Sweatt J.D., Kandel E.R.;
 RT "Long-term sensitization training in Aplysia leads to an increase in
 calreticulin, a major presynaptic calcium-binding protein.";
 RL Neuron 9:1013-1024(1992).
 DR EMBL: S51239; AAB24569.1; -;
 DR InterPro: IPR000886; ER-target.
 DR InterPro: IPR001580; Calreticulin.
 DR Pfam: PF00262; calreticulin; 1.
 DR PRINTS; PR00626; Calreticulin.
 DR ProDom: PD001866; Calreticulin; 1.
 DR PROSITE; PS00803; CALRETICULIN_1; 1.
 DR PROSITE; PS00804; CALRETICULIN_2; 1.
 DR PROSITE; PS00805; CALRETICULIN_REPEAT; 3.
 DR PROSITE; PS00014; ER-TARGET; UNKNOWN_1.
 SQ SEQUENCE 405 AA; 46738 MW; 14CAA201840D1D69 CRC64;

Query Match 82.8%; Score 804; DB 5; Length 405;
 Best Local Similarity 79.4%; Pred. No. 2.3e-68;
 Matches 143; Conservative 18; Mismatches 17; Indels 2; Gaps 1;

QY 1 EPAYYFKEQFLDGDGWTSRWIESKHKSDGKFLVSSGKFGYDEKDKGLQTSODARFYAL 60
 DB 16 DPVYFKEEF--GDDNAERWESKHKSDGKFLVSSGKFGYDEKDKGLQTSODARFYGL 73
 QY 61 SASFEPFSNKGQTLVQFTVKHQNIDCGGYYKFLPNSLDQTDHMGDSYINMFGPDIC 120
 DB 74 SAKFDKFSNEGKTLVQFTVKHQNIDCGGYYKFLPNSLDQTDHMGDSYINMFGPDIC 133
 QY 121 GPOTKKVHVIFNYKGNVLINKIRCKDDDEFTHTLYTLIVRPDNTYEVKIDNSQVESGSLE 180
 DB 134 GPCTKKVHVIFNYKGNVLINKIRCKDDDEFTHTLYTLIVRPDNTYEVKIDNSQVESGSLE 193

RESULT 3
 Q91711 ID Q91711 PRELIMINARY; PRT; 343 AA.
 AC Q91711;
 DT 01-JAN-1998 (Tremblrel. 05, Created)
 DT 01-JAN-1998 (Tremblrel. 05, Last sequence update)
 DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)
 DE CALRETICULIN (FRAGMENT).
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;

OC Xenopodinae; Xenopus.
 OX NCBI_TaxID=8355;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-93074997; PubMed-1445218;
 RA Treves S., Zorzato F., Pozzan T.;
 RT "Identification of calreticulin isoforms in the central nervous
 system.";
 RL Biochem. J. 287:579-581(1992).
 DR EMBL: X67598; CAA47867.1; -;
 DR InterPro: IPR001580; Calreticulin.
 DR Pfam: PF00262; calreticulin; 1.
 DR PRINTS; PR00626; Calreticulin.
 DR ProDom: PD001866; Calreticulin; 1.
 DR PROSITE; PS00803; CALRETICULIN_1; 1.
 DR PROSITE; PS00804; CALRETICULIN_2; 1.
 DR PROSITE; PS00805; CALRETICULIN_REPEAT; 3.
 FT NON_TER 1
 FT NON_TER 343 343
 SQ SEQUENCE 343 AA; 40105 MW; 3E7DDAFA33B91DE1 CRC64;

Query Match 82.1%; Score 797; DB 13; Length 343;
 Best Local Similarity 85.2%; Pred. No. 8.7e-68;
 Matches 144; Conservative 12; Mismatches 13; Indels 0; Gaps 0;

QY 12 DGDGWTSRWIESKHKSDGKFLVSSGKFGYDEKDKGLQTSODARFYALSASFESNKG 71
 DB 1 DGDGWTQWRWESKHKSDGKFLVSSGKFGYDEKDKGLQTSODARFYAMSSRFSNKG 60
 QY 72 QTLVVOFTVKHQNIDCGGYYKFLPNSLDQTDHMGDSYINMFGPDICGPTKKVHVIF 131
 DB 61 QTLVVOFTVKHQNIDCGGYYKFLPNSLDQTDHMGDSYINMFGPDICGPTKKVHVIF 120
 QY 132 NYGKNVLINKIRCKDDDEFTHTLYTLIVRPDNTYEVKIDNSQVESGSLE 180
 DB 121 QYAKKMLQINKIRCKDDDEFTHTLYTLIVRPDNTYEVKIDNSQVESGSLE 169

RESULT 4
 Q98984 ID Q98984 PRELIMINARY; PRT; 419 AA.
 AC Q98984;
 DT 01-FEB-1997 (Tremblrel. 02, Created)
 DT 01-FEB-1997 (Tremblrel. 02, Last sequence update)
 DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)
 DE CALRETICULIN.
 OS Rana rugosa (Frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranidae; Rana.
 OX NCBI_TaxID=8410;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-96234004; PubMed-8654561;
 RA Yamamoto S., Nakamura M.;
 RT "Calnexin: its molecular cloning and expression in the liver of the
 frog, Rana rugosa.";
 RL FEBS Lett. 387:27-32(1996).
 DR [2]
 RP SEQUENCE FROM N.A.
 RA Yamamoto S.;
 RT "Strong expression of the calreticulin gene in the liver of Rana
 rugosa tadpoles.";
 RL J. Exp. Zool. 261:1-10(1996).
 DR EMBL: D78589; BAA11425.1; -;
 DR InterPro: IPR000886; ER-target.
 DR InterPro: IPR001580; Calreticulin.
 DR Pfam: PF00262; calreticulin; 1.
 DR PRINTS; PR00626; Calreticulin.
 DR ProDom: PD001866; Calreticulin; 1.
 DR PROSITE; PS00803; CALRETICULIN_1; 1.
 DR PROSITE; PS00804; CALRETICULIN_2; 1.

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DR PROSITE; PS00805; CALRETICULIN_REPEAT; 3.
DR PROSITE; PS00014; ER_TARGET; UNKNOWN_1.
SQ SEQUENCE 419 AA; 48658 MW; 2C857036769673BF CRC64;

Query Match      82.0%; Score 796; DB 13; Length 419;
Best Local Similarity 80.6%; Pred. No. 1.4e-67;
Matches 145; Conservative 19; Mismatches 16; Indels 0; Gaps 0;

QY 1 EPAYPKEQLDGDGWTSRWIESKHKSDFGKFVLSSSGFYDGDEEKDKGLQTSQDAEFVAL 60
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
19 KPAVYFOEFGCDGDAWKERWIQSCHKSDYGQFKLSACKGFYDGDEEKDKGLQTSQDAKFVAH 78
QY 61 SASPEPSNGQTLLVQFTVKYHEONIDCGGYVKLFPPNSLDOTDMHGDSSEYNIMFPGDIC 120
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
79 SAGFAPEFSNKKDLPLVQGVSVKHEONIDCGGYVKLFPSTLEQTOMHGESEYNIMFPGDIC 138
QY 121 GPCTKKVHVIFNYKGKNVLNKDIRCKDDETHLYTLTVRPDNTYEYKIDNSQVESGSLE 180
Db |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
139 GPPTKKVHVIFNYKGKNLQINKDIRSKADVSHLYTLTVRPDNTYEYKIDNSKVESGNLE 198

RESULT 5
Q9PUC1 PRELIMINARY; PRT; 417 AA.
ID Q9PUC1 AC Q9PUC1;
DT 01-MAY-2000 (T-EMBLrel. 13, Created)
DT 01-MAY-2000 (T-EMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (T-EMBLrel. 17, Last annotation update)
DE CALRETICULIN.
OS Brachydanio rerio (zebrafish) (Zebra danio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
OC Cypriniformes; Cyprinidae; Rasborinae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RA Rubinstein A.L., Lee D., Luo R., Henion P.D., Halpern M.E.;
RT "Genes Dependent on Zebrafish cyplos Function Identified by AFLP
RT Differential Gene Expression Screen.";
RL Genesis 0:0-0(1999);
DR EMBL; AF195882; AAF13700.1; -.
DR InterPro; IPR000886; ER_target.
DR InterPro; IPR001580; Calreticulin.
DR Pfam; PF00262; calreticulin; 1.
DR PRINTS; PR00626; CALRETICULIN.
DR ProDom; PD001866; Calreticulin; 1.
DR PROSITE; PS00803; CALRETICULIN_1; 1.
DR PROSITE; PS00804; CALRETICULIN_2; 1.
DR PROSITE; PS00805; CALRETICULIN_REPEAT; 3.
DR PROSITE; PS00014; ER_TARGET; UNKNOWN_1.
SQ SEQUENCE 417 AA; 48723 MW; 2000C5B4004699B6 CRC64;

Query Match      80.8%; Score 785; DB 13; Length 417;
Best Local Similarity 79.7%; Pred. No. 1.5e-66;
Matches 141; Conservative 19; Mismatches 17; Indels 0; Gaps 0;

QY 4 VYPKEQLDGDGWTSRWIESKHKSDFGKFVLSSSGFYDGDEEKDKGLQTSQDAEFVALSAS 63
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
21 VYPKEQLDGDGWSRVESKHKSDYGQWLTKSGKFYGPDELKDGLQTSQDAEFVALSSR 80
QY 64 FEPSNKGQTLVQFTVKYHEONIDCGGYVKLFPPNSLDOTDMHGDSSEYNIMFPGDICGP 123
Db |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
81 FDSFSNGKGLTVQFTVKYHEONIDCGGYVKVFPAEMDOTMHGESYYIMFPGPICYS 140
QY 124 TKKHVVIFNYKGKNVLNKDIRCKDDETHLYTLTVRPDNTYEYKIDNSQVESGSLE 180
Db |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
141 TKKHVVIFNYKGQNHLNKKDKCKDDELTHLYTLTVRPDNTYEYKIDNEKVESGSLE 197

RESULT 6
Q16893
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RP SEQUENCE FROM N.A.
RA Susan J.M., Just M.L., Lennarz W.J.;
RT "Cloning and Characterization of AlphaP Integrin and Calreticulin in
RL Embryos of the Sea Urchin.";
RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF177915; AAD55725.1; -.
DR InterPro; IPR000886; ER.target.
DR Pfam; PF00262; calreticulin; 1.
DR PRINTS; PR00626; CALRETICULIN.
DR ProDom; PD001866; Calreticulin; 1.
DR PROSITE; PS00804; CALRETICULIN_2; 1.
DR PROSITE; PS00805; CALRETICULIN_REPEAT; 3.
DR PROSITE; PS00014; ER_TARGET; UNKNOWN_1.
KW Signal.
FT SIGNAL.
FT CHAIN.
FT SIGNAL.
FT CHAIN.
SQ SEQUENCE 421 AA; 48822 MW; 172C664F59F41F93 CRC64;

Query Match 75.3%; Score 731; DB 5; Length 421;
Best Local Similarity 74.7%; Pred. No. 2.1e-61;
Matches 133; Conservative 19; Mismatches 24; Indels 2; Gaps 2;

QY 4 VYFKEQFLDGDGWTSRWIESKHK-SDFGKFLVSSGKFGYDEEKDKGLQTSQDARFYALSA 62
DB 20 VYFEDQFADA-SWESRWVESVHKSGDAGKFKWSAGKFGYDAEQDKGIQTSQAKFYGLSA 78
QY 63 SPEPFSNKQGLTVQFTVKRHEQNIDCGGKGYVKLFPPNSLQDTMHGDSSEYNIMFGPDICGP 122
DB 79 KETDFSNEGKDLVQFTVKRHEQNIDCGGKGYKIFPADLQDQMHGDSYNYIMFGPDICGP 138
QY 123 GTKKVVHVFNYGKKNVLINKDKCKDDETHLYTLTVLRPDNTYEVKIDNSQVSGSLE 180
DB 139 GTKKVVHVFNYGKKNLLIKKDKCKDDETHLYTLTVLRKSDNSYEVIRIDNEKAQAGNLE 196

RESULT 8
QY0916
ID QY0916 PRELIMINARY; PRT; 406 AA.
AC QY0916;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE CALRETICULIN.
GN CRC OR CG9429.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-OREGON-R;
RA Dodo K., Sakoyama Y., Gamo S.;
RT "Drosophila melanogaster calreticulin for mRNA.";
RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AH000718; BAA85379.1; -.
DR FlyBase; FBgn0005585; Crc.
DR InterPro; IPR001580; Calreticulin.
DR InterPro; IPR000886; ER.target.
DR Pfam; PF00262; calreticulin; 1.
DR PRINTS; PR00626; CALRETICULIN.
DR ProDom; PD001866; Calreticulin; 1.
DR PROSITE; PS00803; CALRETICULIN_1; 1.
DR PROSITE; PS00804; CALRETICULIN_2; 1.
DR PROSITE; PS00805; CALRETICULIN_REPEAT; 3.
DR PROSITE; PS00014; ER_TARGET; UNKNOWN_1.
SQ SEQUENCE 406 AA; 46809 MW; 68BA49A6B81CC427 CRC64;

Query Match 72.0%; Score 699; DB 5; Length 406;
Best Local Similarity 74.2%; Pred. No. 2.2e-58;

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Matches 132; Conservative 14; Mismatches 30; Indels 2; Gaps 2;

QY 4 VYFKEQFLDGDGWTSRWIESKHK-SDFGKFLVSSGKFGYDEEKDKGLQTSQDARFYALSA 62
DB 21 VYLKENF-DNENWEDPMYISKHPGKFEKFEVLTPTGTFYNDADKGIQTSQARFYAASR 79
QY 63 SPEPFSNKQGLTVQFTVKRHEQNIDCGGKGYVKLFPPNSLQDTMHGDSSEYNIMFGPDICGP 122
DB 80 KEDGFSNEDKPLVQFSVAKHEQNIDCGGKGYVKLFDCSLQDTMHGDSPEYIMFGPDICGP 139
QY 123 GTKKVVHVFNYGKKNVLINKDKCKDDETHLYTLTVLRPDNTYEVKIDNSQVSGSLE 180
DB 140 GTKKVVHVFNYGKKNHLISKDKCKDDVYTHFYTLTVLRPDNTYEVLDNEKVESGNLE 197

RESULT 9
QY0961
ID QY0961 PRELIMINARY; PRT; 403 AA.
AC QY0961;
DT 01-NOV-1998 (TREMBlrel. 08, Created)
DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE CALRETICULIN PRECURSOR.
GN CRT.
OS Necator americanus.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Strongylida;
OC Ancylostomatidae; Ancylostomatidae; Bunostominae; Necator.
OX NCBI_TaxID=51031;
RN [1]
RP SEQUENCE FROM N.A.
RA Pritchard D.I., Brown A., McElroy P., Loukas A., Girdwood K.,
RA Berry C., Fullkrug R., Beck E.;
RT "Calreticulin is a hookworm allergen.";
RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ006790; CAA07254.1; -.
DR InterPro; IPR000886; ER.target.
DR Pfam; PF00262; calreticulin; 1.
DR PRINTS; PR00626; CALRETICULIN.
DR ProDom; PD001866; Calreticulin; 1.
DR PROSITE; PS00803; CALRETICULIN_1; 1.
DR PROSITE; PS00804; CALRETICULIN_2; 1.
DR PROSITE; PS00805; CALRETICULIN_REPEAT; 3.
DR PROSITE; PS00014; ER_TARGET; UNKNOWN_1.
KW Signal; Allergen.
FT SIGNAL.
FT CHAIN.
FT SIGNAL.
FT CHAIN.
SQ SEQUENCE 403 AA; 46833 MW; 21F38B0515487B6F CRC64;

Query Match 70.2%; Score 681.5; DB 5; Length 403;
Best Local Similarity 68.5%; Pred. No. 9.8e-57;
Matches 122; Conservative 30; Mismatches 23; Indels 3; Gaps 3;

QY 4 VYFKEQFLDGDGWTSRWIESKHK-SDFGKFLVSSGKFGYDEEKDKGLQTSQDARFYALSA 63
DB 18 VYFKEEFLD-DSWKEKRWOSKHKSDYGEFVLSAGKFGDATRDQGMKTSQDAKIFYRAAK 76
QY 64 F-EPPFSNKQGLTVQFTVKRHEQNIDCGGKGYVKLFPPNSLQDTMHGDSSEYNIMFGPDICGP 122
DB 77 FPKAFSNKGTVVQFTVKRHEQNIDCGGKGYVKVMSDDVLSDFHGETPYNVNFGPDICGP 136
QY 123 GTKKVVHVFNYGKKNVLINKDKCKDDETHLYTLTVLRPDNTYEVKIDNSQVSGSLE 180
DB 137 -TKKVHDIYSYKGNHLIKKDKCKDDETHLYTLTVLRPDNTYEVQIDGKVESGSE 193

RESULT 10
QY07372
ID QY07372 PRELIMINARY; PRT; 387 AA.
AC QY07372;
DT 01-MAY-1999 (TREMBlrel. 10, Created)
DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)

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DE CALRETICULIN PRECURSOR.
OS Dirofilaria immitis.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea;
OC Onchocercidae; Dirofilaria.
OX NCBI_TaxID=6287;
RN [1]
RP
RX MEDLINE=99094497; PubMed=9879888;
RA Tsuji N., Morales T.H., Ozols V.V., Carmody A.B., Chandrashekar R.;
RT "Molecular characterization of a calcium-binding protein from the
RT filarial parasite Dirofilaria immitis.";
RL Mol. Biochem. Parasitol. 97:69-79(1998).
DR EMBL; AF052978; AD03405.1; -.
DR InterPro; IPR001580; Calreticulin.
DR Pfam; PF00262; calreticulin; 1.
DR PRINTS; PR00626; CALRETICULIN.
DR ProDom; PD001866; Calreticulin; 1.
DR PROSITE; PS00803; CALRETICULIN_1; 1.
DR PROSITE; PS00804; CALRETICULIN_2; 1.
DR PROSITE; PS00805; CALRETICULIN_REPEAT; 3.
KW SIGNAL.
FT CHAIN 1 18 POTENTIAL.
FT CHAIN 19 387 CALRETICULIN.
FT SEQUENCE 387 AA; 44941 MW; E77418F6AFA5885 CRC64;

Query Match 70.0%; Score 680; DB 5; Length 387;
Best Local Similarity 68.5%; Pred. No. 1.3e-56;
Matches 122; Conservative 27; Mismatches 27; Indels 2; Gaps 2;

QY 4 VFPEQFLDGDGWTSRWIESKHKSDFGKFLVSSGKFGYDDEKDKGLQTSODARFYALSAS 63
DB 19 IYFKEEFDSD-DWEKRWIKSKHKKDDFGKWEISHGKFGYDAVKDKGLTKTQDAKFYSIGAK 77
QY 64 FEP-FSNKGQTLVQVTVKHEQNDICGGGVYKLFNPSLQDTDMHGDSSEYNIMFGPDICGP 122
DB 78 FKGFSGNKGKSLVQFSVHQEIDCGGVYKLVMSNDVLEDFHGETTPNIMFGPDICGP 137
QY 123 GTRKKVHVIYFKGNKVLINKDKRCKDDETHLYTLVLRPNDTVYEVKIDNSQVSGSLE 180
DB 138 GTRKKVHVIYFKGNHMKIKRCKDDVFTHTLYTLVNSDNTVEYQIDGKAESGELE 195

RESULT 11
O18478 PRELIMINARY; PRT; 375 AA.
AC O18478;
DT 01-JAN-1998 (TREMBLrel. 05, Created)
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
DE RAL-1 PROTEIN (FRAGMENT).
OS Litomosoides sigmodontis.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea;
OC Onchocercidae; Litomosoides.
OX NCBI_TaxID=42156;
RN [1]
RP
RX MacLennan K., Hoffman W.H., Taylor D.W.;
RL Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ001621; CAA04877.1; -.
DR InterPro; IPR001580; Calreticulin.
DR Pfam; PF00262; calreticulin; 1.
DR PRINTS; PR00626; CALRETICULIN.
DR ProDom; PD001866; Calreticulin; 1.
DR PROSITE; PS00803; CALRETICULIN_1; 1.
DR PROSITE; PS00804; CALRETICULIN_2; 1.
DR PROSITE; PS00805; CALRETICULIN_REPEAT; 3.
FT NON_TER 375
FT SEQUENCE 375 AA; 43842 MW; 03F7642FBFF7A5B8 CRC64;

Query Match 69.3%; Score 673; DB 5; Length 375;
Best Local Similarity 68.5%; Pred. No. 5.8e-56;

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Matches 122; Conservative 26; Mismatches 28; Indels 2; Gaps 2;

QY 4 VFPEQFLDGDGWTSRWIESKHKSDFGKFLVSSGKFGYDDEKDKGLQTSODARFYALSAS 63
DB 19 IYFKEEFDSD-DWEKRWIKSKHKKDDFGKWEISHGKFGYDAVKDKGLTKTQDAKFYSIGAK 77
QY 64 FEP-FSNKGQTLVQVTVKHEQNDICGGGVYKLFNPSLQDTDMHGDSSEYNIMFGPDICGP 122
DB 78 FKGFSGNKGKSLVQFSVHQEIDCGGVYKLVMSNDVLEDFHGETTPNIMFGPDICGP 137
QY 123 GTRKKVHVIYFKGNKVLINKDKRCKDDETHLYTLVLRPNDTVYEVKIDNSQVSGSLE 180
DB 138 GTRKKVHVIYFKGNHMKIKRCKDDVFTHTLYTLVNSDNTVEYQIDGKAESGELE 195

RESULT 12
O9D906 PRELIMINARY; PRT; 380 AA.
AC O9D906;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE 1700031L01RIK PROTEIN.
GN 1700031L01RIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP
RX STRAIN=C57BL/6J; TISSUE=TESTIS;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
DR EMBL; AK006582; BAB24660.1; -.
DR MGD; MGI:1920566; 1700031L01RIK.
DR InterPro; IPR001580; Calreticulin.
DR Pfam; PF00262; calreticulin; 2.
DR PRINTS; PR00626; CALRETICULIN.
DR ProDom; PD001866; Calreticulin; 1.
DR PROSITE; PS00803; CALRETICULIN_1; 1.
DR PROSITE; PS00804; CALRETICULIN_2; 1.
DR PROSITE; PS00805; CALRETICULIN_REPEAT; 3.
FT SEQUENCE 380 AA; 44198 MW; B13BC4ADB11B0442 CRC64;

Query Match 66.0%; Score 641; DB 11; Length 380;
Best Local Similarity 65.0%; Pred. No. 6.4e-53;
Matches 115; Conservative 30; Mismatches 32; Indels 0; Gaps 0;

QY 4 VFPEQFLDGDGWTSRWIESKHKSDFGKFLVSSGKFGYDDEKDKGLQTSODARFYALSAS 63
DB 21 VYFEEFLDGERWRNRWVQSTNDSQGFHFRVSSGKFGYDDEKDKGLQTSQNSRFAISAS 80
QY 64 FEPFSNKGQTLVQVTVKHEQNDICGGGVYKLFNPSLQDTDMHGDSSEYNIMFGPDICGP 123
DB 81 FKPFSGNKGKTLVIQYTVKHEQNDICGGGVYKLVMSNDVLEDFHGETTPNIMFGPDICGP 140

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QY 124 TKKVHVFYFNKGNVLINRCKDDETHLYTLVLRPONTYEVKIDNSQVSGSL 180
      ||||| : : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| :
DB 141 IKKVHLYLFFKNYHENKRPCKPCKPCKPCKPCKPCKPCKPCKPCKPCKPCK 197

RESULT 13
Q40040
ID Q40040 PRELIMINARY; PRT; 412 AA.
AC Q40040;
DT 01-NOV-1996 (TRENBLrel. 01, Created)
DT 01-NOV-1996 (TRENBLrel. 01, Last sequence update)
DT 01-JUN-2001 (TRENBLrel. 17, Last annotation update)
DE CALRETICULIN (FRAGMENT).
GN CRH1
OS Hordeum vulgare (Barley).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
OC Triticeae; Hordeum.
OX NCBI_TaxID 4513;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-MOREX; TISSUE-OVARY;
RX MEDLINE-94339696; PubMed-7914763;
RA Chen F., Hayes P.M., Mulroony D., Pan A.;
RT "Identification and characterization of cDNA clones encoding plant
calreticulin in barley.";
RL Plant Cell 6:835-843(1994).
DR EMBL; L27348; AAA32948.1; -.
DR Mendeil; 8546; Horvu; 1166; 8546.
DR InterPro; IPR000886; ER_target.
DR InterPro; IPR001580; Calreticulin.
DR Pfam; PF00262; calreticulin; 1.
DR ProDom; PD001866; Calreticulin; 1.
DR PROSITE; PS00803; CALRETICULIN_1; 1.
DR PROSITE; PS00804; CALRETICULIN_2; 1.
DR PROSITE; PS00805; CALRETICULIN_REPEAT; 2.
DR PROSITE; PS00014; ER_TARGET; UNKNOWN_1.
KW Calcium-binding.
FT NON_TER 1
FT NON_TER 412
FT NON_TER 415
SQ SEQUENCE 412 AA; 47037 MW; 37F6C95D6AA78AB0 CRC64;

Query Match 55.5%; Score 539; DB 10; Length 412;
Best Local Similarity 56.4%; Pred. No. 3.4e-43;
Matches 101; Conservative 31; Mismatches 41; Indels 6; Gaps 3;

QY 4 VYFKEQFLDGDGWTSMWIESKHSD---FGKFLVSSGKFGYDEKDKGLQTSQDARFYAL 60
      ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| :
DB 20 VFQEQKF--EDGWESRWKSEKKNMAGENNHTSGKWHGDAE-DKGIQTSEDYRFYAI 76

QY 61 SASPEFESNKGQTLVQFTVKHEQNLDCGGYVKKLPNSLDQDMHGDSEYNIMFGPDIC 120
      || : |||| : |||| : |||| : |||| : |||| : |||| : |||| :
DB 77 SAEYFESNKKDKTLVQFTVKHEQNLDCGGYVKKLLGGVDQKKFGDTPYGMFGPDIC 136

QY 121 GPQTKKVVHVFYFNKGNVLINRCKDDETHLYTLVLRPONTYEVKIDNSQVSGSL 179
      ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| :
DB 137 GYSTKKVHTILTNGKNHLLKDKVPCETQDLSHVYTLIRPDATYSLILDNEEKQTGSI 195

RESULT 14
Q40041
ID Q40041 PRELIMINARY; PRT; 415 AA.
AC Q40041;
DT 01-NOV-1996 (TRENBLrel. 01, Created)
DT 01-NOV-1996 (TRENBLrel. 01, Last sequence update)
DT 01-JUN-2001 (TRENBLrel. 17, Last annotation update)
DE CALRETICULIN (FRAGMENT).
GN CRH2
OS Hordeum vulgare (Barley).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

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OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
OC Triticeae; Hordeum.
OX NCBI_TaxID-4513;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-MOREX; TISSUE-OVARY;
RX MEDLINE-94339696; PubMed-7914763;
RA Chen F., Hayes P.M., Mulroony D., Pan A.;
RT "Identification and characterization of cDNA clones encoding plant
calreticulin in barley.";
RL Plant Cell 6:835-843(1994).
DR EMBL; L27349; AAA32949.1; -.
DR Mendeil; 8547; Horvu; 1166; 8547.
DR InterPro; IPR000886; ER_target.
DR InterPro; IPR001580; Calreticulin.
DR Pfam; PF00262; calreticulin; 1.
DR ProDom; PD001866; Calreticulin; 1.
DR PROSITE; PS00803; CALRETICULIN_1; 1.
DR PROSITE; PS00804; CALRETICULIN_2; 1.
DR PROSITE; PS00805; CALRETICULIN_REPEAT; 2.
DR PROSITE; PS00014; ER_TARGET; UNKNOWN_1.
KW Calcium-binding.
FT NON_TER 1
FT NON_TER 415
FT NON_TER 415
SQ SEQUENCE 415 AA; 47359 MW; 2897914812FBE33E CRC64;

Query Match 55.5%; Score 539; DB 10; Length 415;
Best Local Similarity 56.4%; Pred. No. 3.4e-43;
Matches 101; Conservative 31; Mismatches 41; Indels 6; Gaps 3;

QY 4 VYFKEQFLDGDGWTSMWIESKHSD---FGKFLVSSGKFGYDEKDKGLQTSQDARFYAL 60
      ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| :
DB 23 VFQEQKF--EDGWESRWKSEKKNMAGENNHTSGKWHGDAE-DKGIQTSEDYRFYAI 79

QY 61 SASPEFESNKGQTLVQFTVKHEQNLDCGGYVKKLPNSLDQDMHGDSEYNIMFGPDIC 120
      || : |||| : |||| : |||| : |||| : |||| : |||| : |||| :
DB 80 SAEYFESNKKDKTLVQFTVKHEQNLDCGGYVKKLLGGVDQKKFGDTPYGMFGPDIC 139

QY 121 GPQTKKVVHVFYFNKGNVLINRCKDDETHLYTLVLRPONTYEVKIDNSQVSGSL 179
      ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| :
DB 140 GYSTKKVHTILTNGKNHLLKDKVPCETQDLSHVYTLIRPDATYSLILDNEEKQTGSI 198

RESULT 15
Q43712
ID Q43712 PRELIMINARY; PRT; 421 AA.
AC Q43712;
DT 01-NOV-1996 (TRENBLrel. 01, Created)
DT 01-NOV-1996 (TRENBLrel. 01, Last sequence update)
DT 01-JUN-2001 (TRENBLrel. 17, Last annotation update)
DE CALCIUM-BINDING PROTEIN PRECURSOR.
GN CRT1
OS Zea mays (Maize).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade;
OC Panicoideae; Andropogoneae; Zea.
OX NCBI_TaxID-4577;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-VAR MERIT; TISSUE-ROOT TIP;
RA Napier R.M., Trueman S., Henderson J., Boyce J.M., Hawes C.R.,
RA Fricker M.D., Venis M.A.;
RL J. Exp. Bot. 46:1603-1613(1995).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE-96309381; PubMed-8704156;
RA Dresselhaus T., Hagel C., Loerz H., Kranz E.;
RT "Isolation of a full-length cDNA encoding calreticulin from a PCR
library of in vitro zygotes of maize.";
RL Plant Mol. Biol. 31:23-34(1996).
DR EMBL; 246772; CAA86728.1; -.

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DR EMBL; X89813; CAA61939.1; -
DR Mendel; I1228; Zeama; I166; I1228.
DR InterPro; IPR000886; ER_target.
DR InterPro; IPR01580; Calreticulin.
DR Pfam; PF00262; calreticulin; 1.
DR PRINTS; PR00626; CALRETICULIN.
DR PRODom; PD001866; Calreticulin; 1.
DR PROSITE; PS00803; CALRETICULIN_1; 1.
DR PROSITE; PS00804; CALRETICULIN_2; 1.
DR PROSITE; PS00805; CALRETICULIN_REPEAT; 2.
DR PROSITE; PS00014; ER_TARGET; UNKNOWN_1.
KW Signal; Calcium-binding.
FT SIGNAL 1 25 POTENTIAL.
FT CHAIN 26 421 CALRETICULIN.
SQ SEQUENCE 421 AA; 48012 MW; 5AAE02B77ED3126D CRC64;

Query Match 55.2%; Score 536; DB 10; Length 421;
Best Local Similarity 56.4%; Pred. No. 6.7e-43;
Matches 101; Conservative 31; Mismatches 41; Indels 6; Gaps 3;

Qy 4 VYFKRQFLDGDGWTSRWIESKHKSD---FGKRVLSGGKFGYGDDEKDKGLQTSQDARFYAL 60
Db 27 VFFQEKF--EDGWESRWYKSEWKKNMAGENWHTSGKNGDAE-DKGIQTSEDYRFYAI 83

Qy 61 SASPEPFSNKGOTLVQFTVKHEQNIIDCGGYVKLFNPNSLDQTMHGDSEYNIMFGPDIC 120
Db 84 SAEYPEFSNKDKTLVLQFSVRKHEQKLDCCGGYVKLLGGDVQDKFGGDTSYSIMFGPDIC 143

Qy 121 GPGTKKVVHVIKNYKGNVLINKDIRCKDETHLYTLIVRPDNTYEVKIDNSQVESGSL 179
Db 144 GYSTRKKVHTILTQDGNHLIRKDVCEPDTQLTHVYTLIRPDATYSILIDNEEKQTGSI 202
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Search completed: January 9, 2002, 15:03:27
Job time: 269 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: January 9, 2002, 15:02:02 ; Search time 43.73 Seconds
(without alignments)
106.258 Million cell updates/sec

Title: US-09-828-000-4
Perfect score: 340
Sequence: 1 TDMHGSEYNMFPGDICGP.....IRCKDDEFTLTYLIVRPN 61
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues
Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR68:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	340	100.0	417	1 A37047	calreticulin precu
2	335	98.5	400	2 S43376	calreticulin, brai
3	335	98.5	416	1 S06763	calreticulin precu
4	335	98.5	416	2 JH0819	calreticulin precu
5	335	98.5	418	1 A34154	calreticulin precu
6	335	98.5	421	2 S36799	calreticulin precu
7	305	89.7	405	1 JH0795	calreticulin precu
8	296	87.1	384	2 S29130	calreticulin (clon
9	293	86.2	406	2 A56637	calreticulin homol
10	288	84.7	411	2 S29129	calreticulin precu
11	287	84.4	419	2 S71343	calreticulin precu
12	261	76.8	336	2 A32507	41K larval antigen
13	242	71.2	393	1 A48573	calreticulin autoa
14	233.5	68.7	395	2 S25851	calreticulin precu
15	207	60.9	416	2 T14554	calreticulin - bee
16	205	60.3	421	2 S58170	calreticulin precu
17	202	59.4	415	2 T10172	calreticulin - cas
18	200	58.8	412	2 T05703	calreticulin - bar
19	200	58.8	415	2 T05705	calreticulin - bar
20	199	58.5	425	2 C96605	calreticulin (Ctrl
21	195	57.4	422	2 T07841	probable calreticu
22	194	57.1	444	2 H86224	hypothetical prote
23	191	56.2	416	2 T16968	calreticulin call
24	190	55.9	389	2 T03691	calreticulin - com
25	123.5	36.3	592	2 I53260	calnexin - human
26	122.5	36.0	546	2 T06415	calnexin - soybean
27	121.5	35.7	592	2 A46673	calnexin precursor
28	120.5	35.4	591	2 B54354	calnexin precursor
29	120.5	35.4	591	2 C54354	calnexin precursor

30	120.5	35.4	593	1 A37273	calnexin precursor
31	115.5	34.0	530	2 JN0597	calnexin-like prot
32	115.5	34.0	540	2 T10892	probable calnexin
33	115.5	34.0	582	2 A46637	calnexin homolog S
34	115.5	34.0	619	2 S40938	hypothetical prote
35	115.5	34.0	622	2 S71342	calnexin precursor
36	108.5	31.9	428	2 T03251	calnexin - maize (
37	108.5	31.9	611	2 A53418	calmeglin precursor
38	108.5	31.9	611	2 A54086	calnexin-t - mouse
39	103.5	30.4	532	2 T49873	calnexin homolog -
40	103	30.3	560	2 S56142	calcium-binding pr
41	90.5	26.6	297	2 S70552	calnexin homolog C
42	77.5	22.8	540	1 JH0470	site-specific DNA-
43	67.5	19.9	457	2 H85013	hypothetical prote
44	67.5	19.9	968	2 T01733	hypothetical prote
45	66	19.4	560	2 S50439	hypothetical prote

ALIGNMENTS

RESULT 1
A37047
calreticulin precursor - human
N:Alternate names: 52K ribonucleoprotein autoantigen Ro/SS-A; 60K integrin-binding pr
C:Species: Homo sapiens (man)
C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 18-Feb-2000
R:McCaulliffe, D.P.; Yang, Y.S.; Wilson, J.; Sontheimer, R.D.; Capra, J.D.
A:Accession: A42330; A37047; A46452; A28812; PH1525; A40346; S11475; T45075
J. Biol. Chem. 267, 2557-2562, 1992
A:Title: The 5'-flanking region of the human calreticulin gene shares homology with t
A:Reference number: A42330; MUID:92129342
A:Accession: A42330
A:Molecule type: DNA
A:Residues: 1-417 <MC>
A:Note: sequence extracted from NCBI backbone (NCBIN:78537, NCBIP:78536)
R:McCaulliffe, D.P.; Lux, F.A.; Lieu, T.S.; Sanz, I.; Hanke, J.; Newkirk, M.M.; Bachin
J. Clin. Invest. 85, 1379-1391, 1990
A:Title: Molecular cloning, expression, and chromosome 19 localization of a human Ro/
A:Reference number: A37047; MUID:90237213
A:Accession: A37047
A:Molecule type: mRNA
A:Residues: 1-417 <MC>
A:Cross-references: GB:M32294; NID:g337486; PIDN:AAA36582.1; PID:g337487
A:Note: the authors translated the codon GTA for residue 349 as Tyr
R:Rocheach, L.A.; Haselby, J.A.; Meilof, J.F.; Smeenk, R.J.; Unnasch, T.R.; Greene, B.
J. Immunol. 147, 3031-3039, 1991
A:Title: Characterization of the autoantigen calreticulin.
A:Reference number: A46452; MUID:92013129
A:Accession: A46452
A:Molecule type: mRNA
A:Residues: 1-417 <ROK>
A:Cross-references: GB:M84739; NID:g179881; PIDN:AAA51916.1; PID:g179882
A:Note: sequence extracted from NCBI backbone (NCBIN:60749, NCBIP:60750)
R:Lieu, T.S.; Newkirk, M.M.; Capra, J.D.; Sontheimer, R.D.
J. Clin. Invest. 82, 96-101, 1988
A:Title: Molecular characterization of human Ro/SS-A antigen. Amino terminal sequence
A:Reference number: A28812; MUID:88273610
A:Accession: A28812
A:Molecule type: protein
A:Residues: 18-41 <LIE>
A:Note: 18-Ala was also found
R:Dupaix, M.; Schaefer, E.; Krause, K.H.; Tschopp, J.
J. Exp. Med. 177, 1-7, 1993
A:Title: The calcium-binding protein calreticulin is a major constituent of lytic gra
A:Reference number: PH1525; MUID:93115648
A:Accession: PH1525
A:Molecule type: protein
A:Residues: 18-27 <DUP>
A:Experimental source: LAK cell
R:Kojima, M.V.; Finlay, B.B.; Gray, V.; Dedhar, S.
Biochemistry 30, 9859-9866, 1991
A:Title: In vitro interaction of a polypeptide homologous to human Ro/SS-A antigen (c

A:Reference number: A40346; MUID:92002034
 A:Accession: A40346
 A:Molecule type: protein
 A:Residues: 18-34, 'R' <ROU>
 R:Krause, K.H.; Simmerman, H.K.B.; Jones, L.R.; Campbell, K.P.
 Biochem. J. 270, 545-548, 1990
 A:Title: Sequence similarity of calreticulin with a Ca(2+)-binding protein that co-purifies with the endoplasmic reticulum chaperone BiP
 A:Reference number: S11475; MUID:90380058
 A:Accession: S11475
 A:Molecule type: protein
 A:Residues: 18-32 <KRA>
 R:Lamerdin, J.; McCreedy, P.; Stilwagen, S.; Ramirez, M.; Carrano, A.
 submitted to the EMBL Data Library, November 1996
 A:Description: Characterization by genomic sequence analysis of a gene-rich 111 kb region on human chromosome 12p13
 A:Reference number: Z22906
 A:Accession: T45075
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-417 <LAM>
 A:Cross-references: EMBL:AD000092; PIDN:AAB51176.1
 A:Experimental source: cell line 5H2-B; fibroblast
 C:Comment: Autoantibodies specific for this protein are found in Sjogren's syndrome and related autoimmune diseases
 C:Genetics:
 A:Gene: GDB:CALR
 A:Cross-references: GDB:125179; OMIM:109091
 A:Map position: 19p13.3-19p13.2
 A:Introns: 31/1; 65/1; 133/1; 164/3; 234/3; 272/3; 320/3; 351/3
 A:Note: CRTC
 C:Superfamily: calreticulin
 C:Keywords: calcium binding; integrin binding
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 F:18-417/Product: calreticulin #status predicted <MAT>
 F:414-417/Region: endoplasmic reticulum retention signal

Query Match 100.0%; Score 340; DB 1; Length 417;
 Best Local Similarity 100.0%; Pred. No. 4.5e-33;
 Matchew 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TDMHGDSEYNMFPGDTCGPGTKKVVHVFYKGNVLYNKDCKDETHLYTLIVRPD 60
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 DB 120 TDMHGDSEYNMFPGDTCGPGTKKVVHVFYKGNVLYNKDCKDETHLYTLIVRPD 179

QY 61 N 61
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 DB 180 N 180

RESULT 2
 S43376
 calreticulin, brain isoform 1 - bovine
 C:Species: Bos primigenius taurus (cattle)
 C:Date: 20-Oct-1994 #sequence_revision 23-Mar-1995 #text_change 07-May-1999
 A:Accession: S43376; S36801
 R:Matsumoto, K.; Seta, K.; Yamakawa, Y.; Okuyama, T.; Shinoda, T.; Isobe, T.
 Biochem. J. 298, 435-442, 1994
 A:Title: Covalent structure of bovine brain calreticulin.
 A:Reference number: S43376; MUID:94183174
 A:Accession: S43376
 A:Molecule type: protein
 A:Residues: 1-400 <MAT>
 A:Experimental source: brain
 R:Liu, N.; Fine, R.E.; Johnson, R.J.
 Biochim. Biophys. Acta 1202, 70-76, 1993
 A:Title: Comparison of cDNAs from bovine brain coding for two isoforms of calreticulin.
 A:Reference number: S36799; MUID:93385184
 A:Accession: S36801
 A:Status: nucleic acid sequence not shown
 A:Molecule type: mRNA
 A:Residues: 45-63, 'E', 65-83 <LIU>
 A:Experimental source: brain, clone 8.1
 C:Superfamily: calreticulin
 C:Keywords: calcium binding; glycoprotein

F:397-400/Region: endoplasmic reticulum retention signal
 F:120-146/Disulfide bonds: #status experimental
 F:162/Binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match 98.5%; Score 335; DB 2; Length 400;
 Best Local Similarity 98.4%; Pred. No. 1.7e-32;
 Matches 60; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TDMHGDSEYNMFPGDTCGPGTKKVVHVFYKGNVLYNKDCKDETHLYTLIVRPD 60
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 DB 103 TDMHGDSEYNMFPGDTCGPGTKKVVHVFYKGNVLYNKDCKDETHLYTLIVRPD 162

QY 61 N 61
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 DB 163 N 163

RESULT 3
 S06763
 calreticulin precursor - mouse
 N:Alternate names: 55K calcium-binding reticuloplasmin; calregulin
 C:Species: Mus musculus (house mouse)
 C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
 C:Accession: S06763; JCL444; PCL233; A57498
 R:Smith, M.J.; Koch, G.L.E.
 EMBO J. 8, 3581-3586, 1989
 A:Title: Multiple zones in the sequence of calreticulin (CRP55, calregulin, HACBP), a
 A:Reference number: S06763; MUID:90059955
 A:Accession: S06763
 A:Molecule type: DNA
 A:Residues: 1-416 <SMI>
 A:Cross-references: EMBL:X14926; NID:g50567; PIDN:CAA33053.1; PID:g50568
 R:Mazzarella, R.A.; Gold, P.; Cunningham, M.; Green, M.
 Gene 120, 217-225, 1992
 A:Title: Determination of the sequence of an expressible cDNA clone encoding Erp60/ca
 A:Reference number: JCL444; MUID:93013037
 A:Accession: JCL444
 A:Molecule type: mRNA
 A:Residues: 1-416 <MAZ>
 A:Cross-references: GB:M92988; NID:g193084; PIDN:AAA37569.1; PID:g193085
 A:Accession: PCL233
 A:Molecule type: protein
 A:Residues: 18-41 <MAZ>
 R:White, T.K.; Zhu, Q.; Tanzer, M.L.
 J. Biol. Chem. 270, 15926-15929, 1995
 A:Title: Cell surface calreticulin is a putative mannoside lectin which triggers mouse
 A:Reference number: A57498; MUID:95332280
 A:Accession: A57498
 A:Status: preliminary
 A:Molecule type: protein
 A:Residues: 74-80; 142-151; 186-193 <WHI>
 C:Superfamily: calreticulin
 C:Keywords: calcium binding
 F:1-17/Domain: signal sequence #status predicted <SIG>
 F:18-416/Product: calregulin #status experimental <MAT>
 F:413-416/Region: endoplasmic reticulum retention signal

Query Match 98.5%; Score 335; DB 1; Length 416;
 Best Local Similarity 100.0%; Pred. No. 1.8e-32;
 Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DMHGDSEYNMFPGDTCGPGTKKVVHVFYKGNVLYNKDCKDETHLYTLIVRPD 61
 |||||
 DB 121 DMHGDSEYNMFPGDTCGPGTKKVVHVFYKGNVLYNKDCKDETHLYTLIVRPD 180

RESULT 4
 JH0819
 calreticulin precursor - rat
 N:Alternate names: calcium-binding protein 3
 C:Species: Rattus norvegicus (Norway rat)

C;Date: 30-Sep-1993 #sequence_revision 20-Aug-1994 #text_change 20-Jun-2000
 C;Accession: JH0819; A49176; S11205; PC1109; S45036; S04867; S39372; A34473; S13045
 R;Nakamura, M.; Moriya, M.; Baba, T.; Michikawa, Y.; Yamanobe, T.; Arai, K.; Okinaga, S.
 Exp. Cell Res. 205, 101-110, 1993
 A;Title: An endoplasmic reticulum protein, calreticulin, is transported into the acrosom
 A;Reference number: A49176; MUID:93202172
 A;Accession: JH0819
 A;Molecule type: mRNA
 A;Residues: 1-416 <NAK>
 A;Cross-references: GB:D78308; NID:g1089798; PIDN:BAAL1345.1; PID:g18445572
 A;Accession: A49176
 A;Status: preliminary
 A;Molecule type: protein
 A;Residues: 1-416 <NAK>
 A;Cross-references: GB:D78308; NID:g1089798; PIDN:BAAL1345.1; PID:g18445572
 A;Experimental source: Sprague-Dawley, backmatogenic cells
 A;Note: sequence extracted from NCBI backbone (NCBIN:127639, NCBI:P:127643)
 R;Murthy, K.K.; Banville, D.; Srikanth, C.B.; Carrier, F.; Holmes, C.; Bell, A.; Patel, Y.
 Nucleic Acids Res. 18, 4933, 1990
 A;Title: Structural homology between the rat calreticulin gene product and the Onchocerc
 A;Reference number: S11205; MUID:90370496
 A;Accession: S11205
 A;Molecule type: mRNA
 A;Residues: 1-416 <NAK>
 A;Cross-references: EMBL:X53363; NID:g55854; PIDN:CAA37446.1; PID:g55855
 R;Nakamura, M.; Michikawa, Y.; Baba, T.; Okinaga, S.; Arai, K.
 Biochem. Biophys. Res. Commun. 186, 668-673, 1992
 A;Title: Calreticulin is present in the acrosome of spermatids of rat testis.
 A;Reference number: PC1109; MUID:92360010
 A;Accession: PC1109
 A;Molecule type: protein
 A;Residues: 18-32 <NAK2>
 A;Experimental source: Testis, strain Sprague-Dawley
 R;Soennichsen, B.; Fuellekrug, J.; van Nguyen, P.; Diekmann, W.; Robinson, D.G.; Mieskes
 submitted to the EMBL Data Library, May 1994
 A;Description: Retention and retrieval: both mechanisms cooperate to maintain calreticul
 A;Reference number: S45036
 A;Accession: S45036
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-416 <SOE>
 A;Cross-references: EMBL:X79327; NID:g488840; PIDN:CAA55890.1; PID:g488841
 R;Lone, Y.C.; Bailey, A.; Latruffe, N.
 submitted to the EMBL Data Library, December 1988
 A;Reference number: S04867
 A;Accession: S04867
 A;Molecule type: mRNA
 A;Residues: 'R', 270-358, 'AAG' <LON>
 A;Cross-references: EMBL:X13702; NID:g56055; PIDN:CAA31987.1; PID:g930260
 A;Note: the authors designated the protein as D-beta-hydroxybutyrate dehydrogenase
 R;Yokoi, T.; Nagayama, S.; Kajiwara, R.; Kawaguchi, Y.; Horiuchi, R.; Kamataki, T.
 Biochim. Biophys. Acta 1158, 339-344, 1993
 A;Title: Identification of protein disulfide isomerase and calreticulin as autoimmune an
 A;Reference number: S39371; MUID:94072621
 A;Accession: S39372
 A;Molecule type: protein
 A;Residues: 18-23, 'X', 25-32 <YOK>
 R;Van, P.N.; Peter, F.; Soelling, H.D.
 J. Biol. Chem. 264, 17494-17501, 1989
 A;Title: Four intracisternal calcium-binding glycoproteins from rat liver microsomes wit
 tive calcium sequestering rat liver vesicles.
 A;Reference number: A34473; MUID:90008920
 A;Accession: A34473
 A;Status: preliminary
 A;Molecule type: protein
 A;Residues: 18-36 <VAN>
 R;Trevies, S.; de Mattei, M.; Lanfredi, M.; Villa, A.; Green, N.M.; MacLennan, D.H.; Melc
 Biochem. J. 271, 473-480, 1990
 A;Title: Calreticulin is a candidate for a calsequestrin-like function in Ca(2+)-storage
 A;Reference number: S13045; MUID:91054414
 A;Accession: S13045
 A;Molecule type: protein
 A;Residues: 18-29 <TRE>

C;Superfamily: calreticulin
 C;Keywords: calcium binding; glycoprotein
 F:1-17/Domain: signal sequence #status predicted <SIG>
 F:18-416/Product: calreticulin #status experimental <MAT>
 F:204-212/Region: nuclear location signal
 F:413-416/Region: endoplasmic reticulum retention signal
 F:344/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 98.5%; Score 335; DB 2; Length 416;
 Best Local Similarity 100.0%; Pred. No. 1.8e-32;
 Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 DMHGDSEYNIMFGPDICGPGTKKVVHVIYNYGKNVINKDIRCKDDETHLYTLIVRPDN 61
 |||||
 Db 121 DMHGDSEYNIMFGPDICGPGTKKVVHVIYNYGKNVINKDIRCKDDETHLYTLIVRPDN 180
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RESULT 5

A34154
 calreticulin precursor, skeletal muscle - rabbit
 C;Species: Oryctolagus cuniculus (domestic rabbit)
 C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
 C;Accession: A34154; S13047
 R;Fliegel, L.; Burns, K.; MacLennan, D.H.; Reithmeier, R.A.F.; Michalak, M.
 J. Biol. Chem. 264, 21522-21528, 1989
 A;Title: Molecular cloning of the high affinity calcium-binding protein (calreticulin
 A;Reference number: A34154; MUID:90094320
 A;Accession: A34154
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-418 <FLI>
 A;Cross-references: GB:J05138; NID:g164858; PIDN:AAA31188.1; PID:g164859
 R;Trevies, S.; de Mattei, M.; Lanfredi, M.; Villa, A.; Green, N.M.; MacLennan, D.H.; M
 Biochem. J. 271, 473-480, 1990
 A;Title: Calreticulin is a candidate for a calsequestrin-like function in Ca(2+)-stor
 A;Reference number: S13045; MUID:91054414
 A;Accession: S13047
 A;Molecule type: protein
 A;Residues: 19-32 <TRE>
 C;Superfamily: calreticulin
 C;Keywords: skeletal muscle
 F:1-17/Domain: signal sequence #status predicted <SIG>
 F:415-418/Region: endoplasmic reticulum retention signal

Query Match 98.5%; Score 335; DB 1; Length 418;
 Best Local Similarity 100.0%; Pred. No. 1.8e-32;
 Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 DMHGDSEYNIMFGPDICGPGTKKVVHVIYNYGKNVINKDIRCKDDETHLYTLIVRPDN 61
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 Db 121 DMHGDSEYNIMFGPDICGPGTKKVVHVIYNYGKNVINKDIRCKDDETHLYTLIVRPDN 180
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RESULT 6

S36799
 calreticulin precursor, brain isoform 2 - bovine
 C;Species: Bos primigenius taurus (cattle)
 C;Date: 10-Dec-1993 #sequence_revision 23-Mar-1995 #text_change 13-Aug-1999
 C;Accession: S36799; S36800
 R;Liu, N.; Fine, R.E.; Johnson, R.J.
 Biochim. Biophys. Acta 1202, 70-76, 1993
 A;Title: Comparison of cDNAs from bovine brain coding for two isoforms of calreticuli
 A;Reference number: S36799; MUID:93385184
 A;Accession: S36799
 A;Molecule type: mRNA
 A;Residues: 1-421 <LIU>
 A;Cross-references: GB:LI13462; NID:g348693; PIDN:AAC37307.1; PID:g348694
 A;Experimental source: brain, clone 9.4
 A;Accession: S36800
 A;Molecule type: protein
 A;Residues: 35-45 <LI2>

Search completed: January 9, 2002, 15:02:02
Job time: 189 sec

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2	290	29.9	593	1	US-08-296-362-2	Sequence 2, Appli	
3	227	23.4	542	4	US-08-675-816-6	Sequence 6, Appli	
4	89	9.2	660	4	US-09-181-706-8	Sequence 8, Appli	
5	89	9.2	660	4	US-09-458-791-8	Sequence 8, Appli	
6	89	9.2	660	4	US-09-459-066-8	Sequence 8, Appli	
7	77.5	8.0	642	2	US-08-245-511-48	Sequence 48, Appl	
8	77.5	8.0	642	2	US-08-600-993A-48	Sequence 48, Appl	
9	77	7.9	15	3	US-08-946-026-53	Sequence 53, Appl	
10	75	7.7	591	3	US-08-991-408-4	Sequence 4, Appli	
11	75	7.7	1013	2	US-08-866-650-5	Sequence 5, Appli	
12	75	7.7	1013	2	US-09-021-287-5	Sequence 5, Appli	
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17	72.5	7.5	1484	3	US-08-940-086A-56	Sequence 56, Appl	
18	72	7.4	263	1	US-08-152-922A-5	Sequence 5, Appli	
19	72	7.4	511	1	US-08-480-604A-20	Sequence 20, Appl	
20	72	7.4	511	2	US-08-405-496A-20	Sequence 20, Appl	
21	72	7.4	511	4	US-08-915-136-20	Sequence 20, Appl	
22	72	7.4	608	1	US-08-480-604A-21	Sequence 21, Appl	
23	72	7.4	608	2	US-08-405-496A-21	Sequence 21, Appl	
24	72	7.4	608	4	US-08-915-136-21	Sequence 21, Appl	
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Qy	62	ASPEPFSNKGQTLVVQFTVKRHEQINDCGGYVKFLFNSLDQTDMMHGDSEYNFMFGPDIG	121
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Qy	122	PGTKKV-HVIFN-----YKGKNVLINKDIRCKDDETHLYTLIVRP	161
Db	549	PACKVVPHTTFDIIIEQYNELDDIIKLPSQPIFGSPGVKWFEDIKENEHREVRIVFIKE	608
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Db      549   PACKVVPHTTFDIIIEQYNELDDIIRKLPSQPIFEGPFGVKWFDIKENEHREYRIYFIKE 608
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      RESULT          5
US-09-458-791-8
; Sequence 8, Application US/09458791
; Patent No. 6174689
; GENERAL INFORMATION:
; APPLICANT: Spriggs, Melanie
; TITLE OF INVENTION: VIRAL ENCODED SEMAPHORIN PROTEIN
; RECEPTOR DNA AND POLYPEPTIDES
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Janis C. Henry
; STREET: 51 University St.
; CITY: Seattle
; STATE: WA

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;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/09/459,066
;; FILING DATE:
;; CLASSIFICATION:
;; PRIOR APPLICATION DATA: 08/958,598
;; FILING DATE:
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Henry, Junis C
;; REGISTRATION NUMBER: 34,347
;; REFERENCE/DOCKET NUMBER: 2631
;; TELEPHONE: (206)470-4189
;; TELEFAX: (206)233-0644
;; INFORMATION FOR SEQ ID NO: 8:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 660 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
US-09-459-066-8

Query Match 9.2%; Score 89; DB 4; Length 660;
Best Local Similarity 20.6%; Pred. No. 0.14;
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DB 448 YIAQMCINDEGGPSS-LSSHRWSTFLKVELECDIDGRSYRQIHSKAIKTDNDTILYVFF 506
QY 62 ASPEPESNKGQTLVQFTVKHQNDICGGYVKLPFNSLDQTDHMGDSEYNIMFGPDICG 121
DB 507 DS--PYKSALCTYSNNAIKHSEFSKLGYYTKQLPSP-----APGICL 548
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DB 549 PAKGVVPHFTFDIEQYNELDDIIPKLSQPIFEGPSGVKWFEDIKENEHREYRIVFIKE 608
QY 162 DNTYEVKIDNSQVSGSLE 180
DB 609 NTIYSFDTKSKQTRSAQVD 627

RESULT 7
US-08-245-511-48
; Sequence 48, Application US/08245511
; Patent No. 5928900
; GENERAL INFORMATION:
; APPLICANT: Masure, H Robert
; APPLICANT: Pearce, Barbara J
; APPLICANT: Tuomanen, Elaine
; TITLE OF INVENTION: BACTERIAL EXPORTED PROTEINS AND
; NUMBER OF SEQUENCES: 58
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klauber & Jackson
; STREET: 411 Hackensack Avenue
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/245,511
; FILING DATE: 18-MAY-1994
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/116,541

;; FILING DATE: 01-SEP-1994
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Jackson Esq., David A.
;; REGISTRATION NUMBER: 26,742
;; REFERENCE/DOCKET NUMBER: 600-1-069 CIP
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 201 487-5800
;; TELEFAX: 201 343-1684
;; TELEX: 133521
;; INFORMATION FOR SEQ ID NO: 48:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 642 amino acids
;; TYPE: amino acid
;; TOPOLOGY: unknown
;; MOLECULE TYPE: peptide
;; HYPOTHETICAL: NO
;; ANTI-SENSE: NO
;; ORIGINAL SOURCE:
;; ORGANISM: Streptococcus pneumoniae
;; IMMEDIATE SOURCE:
;; CLONE: am1A
;; FEATURE:
;; OTHER INFORMATION: NOTE: the reference contains a
;; sequence error; the correct sequence shown below is obtain
;; OTHER INFORMATION: from GENBANK
;; PUBLICATION INFORMATION:
;; AUTHORS: Alloung, et al.
;; JOURNAL: Mol. Microbiol.
;; VOLUME: 4
;; PAGES: 633-644
;; DATE: 1990
US-08-245-511-48
Query Match 8.0%; Score 77.5; DB 2; Length 642;
Best Local Similarity 21.2%; Pred. No. 2.6;
Matches 42; Conservative 20; Mismatches 81; Indels 55; Gaps 8;
QY 16 WTSR-----W-----IESKHKSDFGKFLVSSGKFGYDEKDKGLQTSQDARFYALSASF 64
DB 164 WNSKLTYSIFWPLNEEFETSKGSDFAKPTDPTSLLYNGPFLKGLTAKSSVEF----VKN 219
QY 65 EPFSNKGQTLVVQFTVKH-----EQNIDCGG-GYVKLPFNSLDQT---DMHCDSEY 111
DB 220 EQWDRKENVHLDITINLAYYDGDSELESERNFTSGAYSARLYPTSSNYSKVAEYKDNLY 279
QY 112 NIMFGPDICGPGTKKVHVFNYKG-----KNVLINKDIR----- 145
DB 280 YTGSGGIAGLCVNIDRQSYNTSKTTDSEKVVATKKALLINKDFRQALNFALDRSAYSQAI 339
QY 146 -CKDDEFTHLYTLIVRPD 162
DB 340 NGKDGAAALAVRNLFVKPD 357
RESULT 8
US-08-600-993A-48
; Sequence 48, Application US/08600993A
; Patent No. 5981229
; GENERAL INFORMATION:
; APPLICANT: Masure, H Robert
; APPLICANT: Pearce, Barbara J
; APPLICANT: Tuomanen, Elaine
; TITLE OF INVENTION: BACTERIAL EXPORTED PROTEINS AND
; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klauber & Jackson
; STREET: 411 Hackensack Avenue
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601

RESULT 9

QY 126 KVVHVFNYKGNVLI--NKDIRCKDDETHLYTLVLRPDNTYEVK 168
Db 973 EYISI-----GDSVLHFHTDDTINKKGFHRYKSIKIRYPTDTHTKK 1013

RESULT 13

US-08-991-408-2

; Sequence 2, Application US/08991408

; Patent No. 6008017

; GENERAL INFORMATION:

; APPLICANT: ARLETH, ANTHONY J.

; APPLICANT: WILLETT, ROBERT N.

; APPLICANT: ELSHOURBAGY, NABIL A.

; APPLICANT: LI, XIAOTONG

; TITLE OF INVENTION: HUMAN CARDIAC/BRAIN TOLLOID-LIKE

; TITLE OF INVENTION: PROTEIN

; NUMBER OF SEQUENCES: 4

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: RAYNER & PRESTIA

; STREET: P.O. BOX 980

; CITY: VALLEY FORGE

; STATE: PA

; COUNTRY: USA

; ZIP: 19482

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: DOS

; SOFTWARE: FastSeq for Windows Version 2.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/991.408

; FILING DATE:

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 60/034.471

; FILING DATE: 02-JAN-1997

; ATTORNEY/AGENT INFORMATION:

; NAME: PRESTIA, PAUL F

; REGISTRATION NUMBER: 23.031

; REFERENCE/DOCKET NUMBER: ATG-50038

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 610-407-0700

; TELEFAX: 610-407-0701

; TELEX: 846169

; INFORMATION FOR SEQ ID NO: 2:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 1013 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: protein

US-08-991-408-2

Query Match

Best Local Similarity 7.7%; Score 75; DB 3; Length 1013;

Matches 33; Conservative 15; Mismatches 39; Indels 18; Gaps 7;

QY 68 SNKGQTLVVQF-TVKHEQNIDCGGYVVKLFPPNSLDOTDMHGDSEYNIMFGPDICGPG-TK 125

Db 923 SERGSRLELSFQTFEEVEEADCGYDVELF-DGLDSTAV-GLGRF-----CGSGPPE 972

QY 126 KVVHVFNYKGNVLI--NKDIRCKDDETHLYTLVLRPDNTYEVK 168

Db 973 EYISI-----GDSVLHFHTDDTINKKGFHRYKSIKIRYPTDTHTKK 1013

RESULT 14

US-09-240-473-5

; Sequence 5, Application US/09240473

; Patent No. 6297011

; GENERAL INFORMATION:

; APPLICANT: Greenspan, Daniel S

; APPLICANT: Takahara, Kazuhiko
; APPLICANT: Hoffman, Guy G
; TITLE OF INVENTION: Mammalian Tolloid-Like Protein
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Quarles & Brady
; STREET: 1 South Pinckney Street
; CITY: Madison
; STATE: WI
; COUNTRY: US
; ZIP: 53703

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/240.473

; FILING DATE:

; CLASSIFICATION:

; ATTORNEY/AGENT INFORMATION:

; NAME: Berson, Bennett J

; REGISTRATION NUMBER: 37094

; REFERENCE/DOCKET NUMBER: 960296.93839

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 608-251-5000

; TELEFAX: 608-251-9166

; INFORMATION FOR SEQ ID NO: 5:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 1013 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

US-09-240-473-5

Query Match

Best Local Similarity 7.7%; Score 75; DB 4; Length 1013;

Matches 33; Conservative 15; Mismatches 39; Indels 18; Gaps 7;

QY 68 SNKGQTLVVQF-TVKHEQNIDCGGYVVKLFPPNSLDOTDMHGDSEYNIMFGPDICGPG-TK 125

Db 923 SERGSRLELSFQTFEEVEEADCGYDVELF-DGLDSTAV-GLGRF-----CGSGPPE 972

QY 126 KVVHVFNYKGNVLI--NKDIRCKDDETHLYTLVLRPDNTYEVK 168

Db 973 EYISI-----GDSVLHFHTDDTINKKGFHRYKSIKIRYPTDTHTKK 1013

RESULT 15

US-08-231-193A-56

; Sequence 56, Application US/08231193A

; Patent No. 5849895

; GENERAL INFORMATION:

; APPLICANT: Daggett, Lorrie P.

; APPLICANT: Ellis, Steven B.

; APPLICANT: Liaw, Chen W.

; APPLICANT: Lu, Chin-Chun

; TITLE OF INVENTION: HUMAN N-METHYL-D-ASPARTATE RECEPTOR

; NUMBER OF SEQUENCES: 63

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Brown, Martin, Haller & McClain

; STREET: 1660 Union Street

; CITY: San Diego

; STATE: CA

; COUNTRY: U.S.A.

; ZIP: 92101-2926

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/231.193A
; FILING DATE: 20-APR-1994
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/052,459
; FILING DATE: 20-APR-1993
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Seldman, Stephanie
; REGISTRATION NUMBER: 33,779
; REFERENCE/DOCKET NUMBER: 6362-9383
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-238-0999
; TELEFAX: 619-238-0062
; INFORMATION FOR SEQ ID NO: 56:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1484 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-231-193A-56

Query Match 7.5%; Score 72.5; DB 2; Length 1484;
Best Local Similarity 27.7%; Pred. No. 32;
Matches 23; Conservative 13; Mismatches 28; Indels 19; Gaps 4;

QY 45 KDKG--LQTSQDARFYALASPEPFSKQGLVVOFTVKHEQNIDCGGYV---KLEPNS 99
      |||| : | : ||| | : | : | : | : | : | : | : | : | : | :
Db 1325 KDKGRPMGDSFYAHMPMSAGESTFANKSSVP---TAGHHHHNNPPGGYMLSKSLYPDR 1381

QY 100 L-----DQTDHMGDSEY 111
      : || : || :
Db 1382 VTQNPFIPTFGDDQCLLGSKSY 1404
```

Search completed: January 9, 2002, 14:59:42
Job time: 69 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: January 9, 2002, 14:58:53 ; Search time 43.73 Seconds
(without alignments)
313.547 Million cell updates/sec

Title: US-09-828-000-3
Perfect score: 971
Sequence: 1 EPAYPKQFLDGDGWTSRW.....PDNYEVKIDNSQVESGSLE 180
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_68.*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	971	100.0	417	1 A37047	calreticulin precu
2	933	96.1	416	2 JH0819	calreticulin precu
3	931	95.9	418	1 A34154	calreticulin precu
4	930	95.8	400	2 S43376	calreticulin, brai
5	930	95.8	416	1 S06763	calreticulin precu
6	835	86.0	411	2 S29129	calreticulin precu
7	804	82.8	405	1 JH0795	calreticulin (clon
8	797	82.1	384	2 S29130	calreticulin precu
9	796	82.0	419	2 S71343	calreticulin homol
10	699	72.0	406	2 A56637	calreticulin precu
11	619.5	63.8	396	2 S25851	41K larval antigen
12	542.5	55.9	335	2 A32507	calreticulin - bar
13	539	55.5	412	2 T05703	calreticulin - bar
14	539	55.5	415	2 T05705	calreticulin - bar
15	536	55.2	421	2 S58170	calreticulin precu
16	531	54.7	416	2 T14554	calreticulin - bee
17	527	54.3	415	2 T10172	calreticulin - cas
18	522.5	53.8	421	2 S36799	calreticulin precu
19	522	53.8	416	2 T16968	calreticulin call
20	517	53.2	389	2 T03691	calreticulin - com
21	512	52.7	425	2 C96605	calreticulin (Ctrl
22	510	52.5	444	2 H86224	hypothetical prote
23	496	51.1	393	1 A48573	calreticulin autoa
24	347	35.7	422	2 T07841	probable calreticu
25	293	30.2	591	2 B54354	calnexin precursor
26	290	29.9	591	2 C54354	calnexin precursor
27	290	29.9	592	2 I53260	calnexin - human
28	290	29.9	593	1 A47273	calnexin precursor
29	288	29.7	592	2 A46673	calnexin precursor

ALIGNMENTS

RESULT 1
A37047
calreticulin precursor - human
N:Alternate names: 52K ribonucleoprotein autoantigen Ro/SS-A; 60K integrin-binding pr
C:Species: Homo sapiens (man)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 18-Feb-2000
R:Accession: A42330; A37047; A46452; A28812; PH1525; A40346; S11475; T45075
R:McCaulliffe, D.P.; Yang, Y.S.; Wilson, J.; Sontheimer, R.D.; Capra, J.D.
J. Biol. Chem. 267, 2557-2562, 1992
A:Title: The 5'-flanking region of the human calreticulin gene shares homology with t
A:Reference number: A42330; MUID:92129342
A:Accession: A42330
A:Molecule type: DNA
A:Residues: 1-417 <MC2>
A:Note: sequence extracted from NCBI backbone (NCBIN:78537, NCBIP:78536)
R:McCaulliffe, D.P.; Lux, F.A.; Lieu, T.S.; Sanz, I.; Hanke, J.; Newkirk, M.M.; Bachin
J. Clin. Invest. 85, 1379-1391, 1990
A:Title: Molecular cloning, expression, and chromosome 19 localization of a human Ro/
A:Reference number: A37047; MUID:90237213
A:Accession: A37047
A:Molecule type: mRNA
A:Residues: 1-417 <MC2>
A:Cross-references: GB:M32294; NID:g337486; PIDN:AAA36582.1; PID:g337487
A:Note: the authors translated the codon GTA for residue 349 as Tyr
R:Roakech, L.A.; Haselby, J.A.; Mellof, J.F.; Smeenk, R.J.; Unnasch, T.R.; Greene, B.
J. Immunol. 147, 3031-3039, 1991
A:Title: Characterization of the autoantigen calreticulin.
A:Reference number: A46452; MUID:92013129
A:Accession: A46452
A:Molecule type: mRNA
A:Residues: 1-417 <R0K>
A:Cross-references: GB:M4739; NID:g179881; PIDN:AAA51916.1; PID:g179882
A:Note: sequence extracted from NCBI backbone (NCBIN:60749, NCBIP:60750)
R:Lieu, T.S.; Newkirk, M.M.; Capra, J.D.; Sontheimer, R.D.
J. Clin. Invest. 82, 96-101, 1988
A:Title: Molecular characterization of human Ro/SS-A antigen. Amino terminal sequence
A:Reference number: A28812; MUID:88273610
A:Accession: A28812
A:Molecule type: protein
A:Residues: 18-41 <LIE>
A:Note: 18-Ala was also found
R:Dupuis, M.; Schaefer, E.; Krause, K.H.; Tschopp, J.
J. Exp. Med. 177, 1-7, 1993
A:Title: The calcium-binding protein calreticulin is a major constituent of lytic gra
A:Reference number: PH1525; MUID:93115648
A:Accession: PH1525
A:Molecule type: protein
A:Residues: 18-27 <DUP>
A:Experimental source: LAK cell
R:Roiani, M.V.; Finlay, B.B.; Gray, V.; Dedhar, S.
Biochemistry 30, 9859-9866, 1991
A:Title: In vitro interaction of a polypeptide homologous to human Ro/SS-A antigen (c

QY 61 SASFEPPSNKQGLVVOFTVKHEQNIDCGGVYKFLPNSLDQTMHGDSEYNIMFGPDIC 120
 |||||||
 Db 78 SARFEPFSNKGQTLVVQFTVKHEQNIDCGGVYKFLPNSLDQTMHGDSEYNIMFGPDIC 137
 |||||||
 QY 121 GPCTKKVHVIFNYKGNKVLINKIRCKDDETHLYTLIVRPNTYEVKIDNSQVESGSLE 180
 |||||||
 Db 138 GPCTKKVHVIFNYKGNKVLINKIRCKDDETHLYTLIVRPNTYEVKIDNSQVESGSLE 197
 |||||||

RESULT 3
 A34154
 calreticulin precursor, skeletal muscle - rabbit
 C:Species: Oryctolagus cuniculus (domestic rabbit)
 C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
 C:Accession: A34154; S13047
 R:Fliegel, L.; Burns, K.; MacLennan, D.H.; Reithmeier, R.A.F.; Michalak, M.
 J. Biol. Chem. 264, 21522-21528, 1989
 A:Title: Molecular cloning of the high affinity calcium-binding protein (calreticulin) c
 A:Reference number: A34154; MUID:90094320
 A:Accession: A34154
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-418 <FLI>
 A:Cross-references: GB:J05138; NID:g164858; PIDN:AAA31188.1; PID:g164859
 R:Treves, S.; de Mattei, M.; Lanfredi, M.; Villa, A.; Green, N.M.; MacLennan, D.H.; Mel
 Biochem. J. 271, 473-480, 1990
 A:Title: Calreticulin is a candidate for a calsequestrin-like function in Ca(2+)-storage
 A:Reference number: S13045; MUID:91054414
 A:Accession: S13047
 A:Molecule type: protein
 A:Residues: 19-32 <TR>
 C:Superfamily: calreticulin
 C:Keywords: skeletal muscle
 F:1-17/Domain: signal sequence #status predicted <SIG>
 F:415-418/Region: endoplasmic reticulum retention signal

Query Match 95.9%; Score 931; DB 1; Length 418;
 Best Local Similarity 95.6%; Pred. No. 1.3e-76;
 Matches 172; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

QY 1 EPAVYFKEQFLDGDGWTSRWIESKHKSDFGKFLVSSGKFYGDDEKDKGLQTSQDARFYAL 60
 |||||||
 Db 18 EPVYFKEQFLDGDGWTSRWIESKHKSDFGKFLVSSGKFYGDDEKDKGLQTSQDARFYAL 77
 |||||||
 QY 61 SASFEPPSNKQGLVVOFTVKHEQNIDCGGVYKFLPNSLDQTMHGDSEYNIMFGPDIC 120
 |||||||
 Db 78 SARFEPFSNKGQTLVVQFTVKHEQNIDCGGVYKFLPNSLDQTMHGDSEYNIMFGPDIC 137
 |||||||
 QY 121 GPCTKKVHVIFNYKGNKVLINKIRCKDDETHLYTLIVRPNTYEVKIDNSQVESGSLE 180
 |||||||
 Db 138 GPCTKKVHVIFNYKGNKVLINKIRCKDDETHLYTLIVRPNTYEVKIDNSQVESGSLE 197
 |||||||

RESULT 4
 S43376
 calreticulin, brain isoform 1 - bovine
 C:Species: Bos primigenius taurus (cattle)
 C:Date: 20-Oct-1994 #sequence_revision 23-Mar-1995 #text_change 07-May-1999
 C:Accession: S43376; S36801
 R:Matsuoka, K.; Seta, K.; Yamakawa, Y.; Okuyama, T.; Shinoda, T.; Isobe, T.
 Biochem. J. 298, 435-442, 1994
 A:Title: Covalent structure of bovine brain calreticulin.
 A:Reference number: S43376; MUID:94183174
 A:Accession: S43376
 A:Molecule type: protein
 A:Residues: 1-400 <MAT>
 A:Experimental source: brain
 R:Liu, N.; Fine, R.E.; Johnson, R.J.
 Biochim. Biophys. Acta 1202, 70-76, 1993
 A:Title: Comparison of cDNAs from bovine brain coding for two isoforms of calreticulin.
 A:Reference number: S36799; MUID:93385184

A:Accession: S36801
 A:Status: nucleic acid sequence not shown
 A:Molecule type: mRNA
 A:Residues: 45-63, 'E', 65-83 <LIU>
 A:Experimental source: brain, clone 8.1
 C:Superfamily: calreticulin
 C:Keywords: calcium binding; glycoprotein
 F:397-400/Region: endoplasmic reticulum retention signal
 F:120-146/Disulfide bonds: #status experimental
 F:162/Binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match 95.8%; Score 930; DB 2; Length 400;
 Best Local Similarity 95.0%; Pred. No. 1.6e-76;
 Matches 171; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 1 EPAVYFKEQFLDGDGWTSRWIESKHKSDFGKFLVSSGKFYGDDEKDKGLQTSQDARFYAL 60
 |||||||
 Db 1 DPTVYFKEQFLDGDGWTSRWIESKHKSDFGKFLVSSGKFYGDDEKDKGLQTSQDARFYAL 60
 |||||||
 QY 61 SASFEPPSNKQGLVVOFTVKHEQNIDCGGVYKFLPNSLDQTMHGDSEYNIMFGPDIC 120
 |||||||
 Db 61 SARFEPFSNKGQTLVVQFTVKHEQNIDCGGVYKFLPNSLDQTMHGDSEYNIMFGPDIC 120
 |||||||
 QY 121 GPCTKKVHVIFNYKGNKVLINKIRCKDDETHLYTLIVRPNTYEVKIDNSQVESGSLE 180
 |||||||
 Db 121 GPCTKKVHVIFNYKGNKVLINKIRCKDDETHLYTLIVRPNTYEVKIDNSQVESGSLE 180
 |||||||

RESULT 5
 S06763
 calreticulin precursor - mouse
 N:Alternate names: 55K calcium-binding reticuloplasmin; calregulin
 C:Species: Mus musculus (house mouse)
 C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
 C:Accession: S06763; JCI444; PC1233; A57498
 R:Smith, M.J.; Koch, G.L.E.
 EMBO J. 8, 3581-3586, 1989
 A:Title: Multiple zones in the sequence of calreticulin (CRP55, calregulin, HACBP), a
 A:Reference number: S06763; MUID:90059955
 A:Accession: S06763
 A:Molecule type: DNA
 A:Residues: 1-416 <SMI>
 A:Cross-references: EMBL:X14926; NID:g50567; PIDN:CAA33053.1; PID:g50568
 R:Mazzarella, R.A.; Gold, P.; Cunningham, M.; Green, M.
 Gene 120, 217-225, 1992
 A:Title: Determination of the sequence of an expressible cDNA clone encoding Erp60/ca
 A:Reference number: JCI444; MUID:93013037
 A:Accession: JCI444
 A:Molecule type: mRNA
 A:Residues: 1-416 <MAZ>
 A:Cross-references: GB:M92988; NID:g193084; PIDN:AAA37569.1; PID:g193085
 A:Accession: PC1233
 A:Molecule type: protein
 A:Residues: 18-41 <MAZ>
 R:White, T.K.; Zhu, Q.; Tanzer, M.L.
 J. Biol. Chem. 270, 15926-15929, 1995
 A:Title: Cell surface calreticulin is a putative mannose lectin which triggers mous
 A:Reference number: A57498; MUID:95332280
 A:Accession: A57498
 A:Status: preliminary
 A:Molecule type: protein
 A:Residues: 74-80; 142-151; 186-193 <WHI>
 C:Superfamily: calreticulin
 C:Keywords: calcium binding
 F:1-17/Domain: signal sequence #status predicted <SIG>
 F:18-416/Product: calregulin #status experimental <MAT>
 F:413-416/Region: endoplasmic reticulum retention signal

Query Match 95.8%; Score 930; DB 1; Length 416;
 Best Local Similarity 94.4%; Pred. No. 1.6e-76;
 Matches 170; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

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QY 1 EPAVYKKEQFLDGDGWTSMWESKHKSDGKFKVLSGKFGYDEEDKGLQTSODARFYAL 60
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DB 18 DPATYKKEQFLDGDGWTSMWESKHKSDGKFKVLSGKFGYDEEDKGLQTSODARFYAL 77
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 61 SASFPFSSNKGQTLVVOFTVKHEQNDICGGGVYKFLPNSLDQTDHMGDSEYNIMFGPDIC 120
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 78 SAKFPEFSNKGQTLVVOFTVKHEQNDICGGGVYKFLPNSLDQTDHMGDSEYNIMFGPDIC 137
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 121 GPCTKKVHVIFNYKGNKVLNIDCKDDKDEFTHLTYTLIVRPNTYEVKIDNSQVSGSLE 180
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 138 GPCTKKVHVIFNYKGNKVLNIDCKDDKDEFTHLTYTLIVRPNTYEVKIDNSQVSGSLE 197
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
RESULT 6
S29129
C:Species: Xenopus laevis (African clawed frog)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 13-Aug-1999
C:Accession: S29129
R:Trevies, S.; Zorzato, F.; Pozzan, T.
Biochem. J. 287, 579-581, 1992
A:Title: Identification of calreticulin isoforms in the central nervous system.
A:Reference number: S29129; MUID:93074997
A:Accession: S29129
A:Molecule type: mRNA
A:Residues: 1-411 <TRE>
A:Cross-references: EMBL:X67597; NID:g64608; PIDN:CAA47866.1; PID:g64609
C:Superfamily: calreticulin
C:Keywords: glycoprotein
F:1-12/Domain: signal sequence (fragment) #status predicted <SIG>
F:13-411/Product: calreticulin #status predicted <MAT>
F:408-411/Region: endoplasmic reticulum retention signal
F:339/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 86.0%; Score 835; DB 2; Length 411;
Best Local Similarity 83.9%; Pred. No. 6.2e-68;
Matches 151; Conservative 15; Mismatches 14; Indels 0; Gaps 0;

QY 1 EPAVYKKEQFLDGDGWTSMWESKHKSDGKFKVLSGKFGYDEEDKGLQTSODARFYAL 60
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 13 EPAVYKKEEFTDGDGWTQWESKHKTDGKFKLSAGKFGYDSEKDKGLQTSODARFYAM 72
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 61 SASFPFSSNKGQTLVVOFTVKHEQNDICGGGVYKFLPNSLDQTDHMGDSEYNIMFGPDIC 120
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 73 SSRPDSFSNKGQTLVVOFTVKHEQNDICGGGVYKFLPNSLDQTDHMGDSEYNIMFGPDIC 132
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 121 GPCTKKVHVIFNYKGNKVLNIDCKDDKDEFTHLTYTLIVRPNTYEVKIDNSQVSGSLE 180
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 133 GPPTKKVHVIFQYKKNLQINIDCKDDKDEFTHLTYTLIVRPNTYEVKIDNSQVSGSLE 192
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
RESULT 7
JH0795
calreticulin precursor - California sea hare
N:Alternate names: protein 407
C:Species: Aplysia californica (California sea hare)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C:Accession: JH0795; B31409; F60977
R:Kennedy, T.E.; Kuhl, D.; Barzilai, A.; Sweatt, J.D.; Kandel, E.R.
Neuron 9, 1013-1024, 1992
A:Title: Long-term sensitization training in aplysia leads to an increase in calreticulin
A:Reference number: JH0795; MUID:93098937
A:Accession: JH0795
A:Molecule type: mRNA
A:Residues: 1-405 <KNS>
A:Cross-references: GB:S51239; NID:g262053; PIDN:AAB24569.1; PID:g262054
A:Experimental source: abdominal ganglion and antral nervous system
R:Kennedy, T.E.; Gawinowicz, M.A.; Barzilai, A.; Kandel, E.R.; Sweatt, J.D.
Proc. Natl. Acad. Sci. U.S.A. 85, 7008-7012, 1988
A:Title: Sequencing of proteins from two-dimensional gels by using in situ digestion and
tion in Aplysia.
```

```
A:Reference number: A94207; MUID:88320566
A:Accession: B31409
A:Molecule type: protein
A:Residues: 'X',17-28,'X',30-31 <KE2>
R:Sweatt, J.D.; Kennedy, T.E.; Wager-Smith, K.; Gawinowicz, M.A.; Barzilai, A.; Karl,
Electrophoresis 10, 152-157, 1989
A:Title: Development of a database of amino acid sequences for proteins identified an
A:Reference number: A60977; MUID:89276264
A:Accession: F60977
A:Molecule type: protein
A:Residues: 'X',17-28,'X',30-31 <SWE>
C:Superfamily: calreticulin
C:Keywords: calcium binding; endoplasmic reticulum
F:1-15/Domain: signal sequence #status predicted <SIG>
F:16-405/Product: calreticulin #status experimental <MAT>
F:402-405/Region: endoplasmic reticulum retention signal

Query Match 82.8%; Score 804; DB 1; Length 405;
Best Local Similarity 79.4%; Pred. No. 3.9e-65;
Matches 143; Conservative 18; Mismatches 17; Indels 2; Gaps 1;

QY 1 EPAVYKKEQFLDGDGWTSMWESKHKSDGKFKVLSGKFGYDEEDKGLQTSODARFYAL 60
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 16 DPTVYFKEEF--GDDWAERWVESKHKSDLGKFKVLTAGKFGYDAEKDKGIQTSDARFYGL 73
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 61 SASFPFSSNKGQTLVVOFTVKHEQNDICGGGVYKFLPNSLDQTDHMGDSEYNIMFGPDIC 120
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 74 SAKFDKFSNEGKTLVQFTVKHEQNDICGGGVYKVFSSDLQSDMHGSESPYIMFGPDIC 133
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 121 GPCTKKVHVIFNYKGNKVLNIDCKDDKDEFTHLTYTLIVRPNTYEVKIDNSQVSGSLE 180
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 134 GPCTKKVHVIFNYKGNKVLNIDCKDDKDEFTHLTYTLIVRPNTYEVKIDNEKESGDLLE 193
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
RESULT 8
S29130
calreticulin (clone 8) - African clawed frog (fragment)
C:Species: Xenopus laevis (African clawed frog)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 13-Aug-1999
C:Accession: S29130; T01068
R:Trevies, S.; Zorzato, F.; Pozzan, T.
Biochem. J. 287, 579-581, 1992
A:Title: Identification of calreticulin isoforms in the central nervous system.
A:Reference number: S29129; MUID:93074997
A:Accession: S29130
A:Molecule type: mRNA
A:Residues: 1-384 <TRE>
A:Cross-references: EMBL:X67598
A:Accession: T01068
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-339,'XTCR' <TRW>
A:Cross-references: EMBL:X67598; NID:g64610; PIDN:CAA47867.1; PID:g64611
A:Experimental source: CNS
C:Superfamily: calreticulin
C:Keywords: glycoprotein
F:381-384/Region: endoplasmic reticulum retention signal
F:316/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 82.1%; Score 797; DB 2; Length 384;
Best Local Similarity 85.2%; Pred. No. 1.6e-64;
Matches 144; Conservative 12; Mismatches 13; Indels 0; Gaps 0;

QY 12 DGDGWTSMWESKHKSDGKFKVLSGKFGYDEEDKGLQTSODARFYALSAPFESNKG 71
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 1 DGDGWTQWVESKHKSDYGKFKLSAGKFGYDSEKDKGLQTSODARFYAMSSRFESNKG 60
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 72 QTLVVOFTVKHEQNDICGGGVYKFLPNSLDQTDHMGDSEYNIMFGPDICGCTKKVHVIF 131
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 61 QTLVVOFTVKHEQNDICGGGVYKFLPADLEQTEMHGESEYNIMFGPDICGPTKKVHVIF 120
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
```

A; Introns: 65/1; 222/3
C; Superfamily: calreticulin
C; Keywords: calcium binding; endoplasmic reticulum
F; 1-17/Domain: signal sequence #status predicted <SIG>
F; 403-406/Region: endoplasmic reticulum retention signal

Query Match 72.0%; Score 599; DB 2; Length 406;
Best Local Similarity 74.2%; Pred. No. 1.2e-55;
Matches 132; Conservative 14; Mismatches 30; Indels 2; Gaps 2;

Qy 4 VFYEQFLDGGWTSRWTESKHK-SDFCKFVLSGKFYGDEEKDKGLQTSDARFYALSA 62
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
Db 21 VYLKENP-DNENWEDTWIYSKHGKEFGKFLVTPTGTFYNDAEADKGITSDARYAASR 79
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
Qy 63 SFEPSNGKGTLVQVOTVKHEQNIDCGGGYVKLPFNSLDQTDHMGDSYNTIMFGPDICGP 122
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
Db 80 KFDGFSNEDKPLVQVFSVKHEQNIDCGGGYVKLFDCLSDQTDHGESPYETMFGPDICGP 139
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
Qy 123 GTKKVHVIFNVKGNVLNKDIRCKDDETHLYTLIVRPDNTYYEVKINDSQVESGSLE 180
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
Db 140 GTKKVHVIFS YKGNHLISKDIRCKDDVVTHFTYTLIVRPDNTYEVLIIDNEKVESGNLE 197
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :

RESULT 11
S25851
calreticulin precursor - Caenorhabditis elegans
C; Species: Caenorhabditis elegans
C; Date: 06-Jan-1994 #sequence_revision 10-Nov-1995 #text_change 05-Nov-1999
C; Accession: S25851; T33996
R; Smith, M.J.
DNA Seq. 2, 235-240, 1992
A; Title: A C. elegans gene encodes a protein homologous to mammalian calreticulin.
A; Reference number: S25851; MUID:92329978
A; Accession: S25851
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-395 <SMI>
A; Cross-references: EMBL:X59589; NID:g6693; PIDN:CAA42159.1; PID:g6694
R; Bauer, C.; Courtney, L.; Laplant, Y.
submitted to the EMBL Data Library, February 1999
A; Description: The sequence of C. elegans cosmid Y38A10A.
A; Reference number: 221453
A; Accession: T33996
A; Status: preliminary; translated from GB/EMBL/DBJ
A; Molecule type: DNA
A; Residues: 1-395 <BAU>
A; Cross-references: EMBL:AF125963; PIDN:AAD14746.1; GSPDB:GN00023; CESP:Y38A10A.5
A; Experimental source: strain Bristol N2; clone Y38A10A
C; Genetics:
A; Gene: CESP:Y38A10A.5
A; Map position: 5
A; Introns: 107/3; 315/3
C; Superfamily: calreticulin
F; 1-15/Domain: signal sequence #status predicted <SIG>
F; 392-395/Region: endoplasmic reticulum retention signal

Query Match 63.8%; Score 619.5; DB 2; Length 395;
Best Local Similarity 63.5%; Pred. No. 1.8e-48;
Matches 113; Conservative 26; Mismatches 36; Indels 3; Gaps 3;

Qy 4 VFYEQFLDGGWTSRWTESKHKSDFGKFVLSGKFYGDEEKDKGLQTSDARFYALSA 63
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
Db 17 VFYKEEFNDA-SWEKRWVOSKHKDDFGAFKLISAGAFFDVESRDQGIQISDAQKFVSRAK 75
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
Qy 64 FE-PFNSNGKGTLVQVOTVKHEQNIDCGGGYVKLPFNSLDQTDHMGDSYNTIMFGPDICGP 122
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
Db 76 FDKDFSNGKTKLVQIYTVKHEQIDCGGGYVKVMRADLDGFHGCTPYNVMFPGPDICGP 135
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
Qy 123 GTKKVHVIFNVKGNVLNKDIRCKDDETHLYTLIVRPDNTYYEVKINDSQVESGSLE 180
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
Db 136 -TRRVHVILNVKGNKLKKTCTSKDELTHLYTLILNSDNTYEVKIDGESAQTSGLE 192
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :

Query Match 55.2%; Score 536; DB 2; Length 421;
Best Local Similarity 56.4%; Pred. No. 6.7e-41;
Matches 101; Conservative 31; Mismatches 41; Indels 6; Gaps 3;
Qy 4 VYKRFQFLDGDGTSRWTESKHSD--FGKFLSSGRFYGDEEKDKGLQTSODARFYAL 60
Db 27 VFFQKRF--EDGWESRWVKSWKKNWAGENNHTSGRWNGDAE--DKGIQTSEDYRFYAI 83
Qy 61 SASPEPFSNKGQTLVVOFTVRKHEQNIDCGGYVKLFPPNSLDQTMHGDSEYNIMEGPDIC 120
Db 84 SAEYPEFSNKDKTLVLQFSVRKHEQKLDGCGGYVKLLGGVDQKKFGGDTYSIMEGPDIC 143
Qy 121 GPGTKKVVHVIENYKGNVLINKDIRCKDDETHLYTLIVRPDNTYEVKIDNSQVESGSL 179
Db 144 GYSTKKVHTILTCKGNHLIRKDVPCETDQLTHVYTLIIRPDATYSILIDNEEKQTGSI 202

Search completed: January 9, 2002, 15:02:02
Job time: 189 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: January 9, 2002, 15:12:15 ; Search time 25.18 Seconds
(without alignments)
50.964 Million cell updates/sec

Title: US-09-828-000-7

Perfect score: 189

Sequence: 1 VFVNYGKNVLINKIRCKDDEPHTLYLIVRPDN 35

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 100059 seqs, 36664827 residues

Total number of hits satisfying chosen parameters: 100059

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_39.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	189	100.0	416	1	CRTC_MOUSE
2	189	100.0	416	1	CRTC_RAT
3	189	100.0	417	1	CRTC_HUMAN
4	189	100.0	418	1	CRTC_RABIT
5	184	97.4	400	1	CRT1_BOVIN
6	184	97.4	421	1	CRT2_BOVIN
7	158	83.6	406	1	CRTC_DROME
8	139	73.5	388	1	RALL_ONCV0
9	138	73.0	393	1	CRTC_SCHMA
10	129	68.3	395	1	CRTC_CAEEL
11	126	66.7	420	1	CRTC_CHLRE
12	110	58.2	416	1	CRTC_BETVU
13	108.5	57.4	424	1	CRTC_DICDI
14	107	56.6	421	1	CRTC_PRUAR
15	105	55.6	415	1	CRTC_RICCO
16	105	55.6	424	1	CRTC_ARATH
17	103	54.5	424	1	CRTC_MAIZE
18	102	54.0	424	1	CRTC_ARATH
19	100	52.9	425	1	CRTL_ARATH
20	98	51.9	424	1	CRTC_ORISA
21	94	49.7	416	1	CRTC_NICPL
22	90.5	47.9	416	1	CRTC_BERST
23	90	47.6	401	1	CRTC_EUGGR
24	64	33.9	540	1	MTAL_ACICA
25	64	33.9	592	1	CALX_HUMAN
26	63	33.3	591	1	CALX_MOUSE
27	63	33.3	591	1	CALX_RAT
28	63	33.3	593	1	CALX_CANFA
29	59	31.2	540	1	CALX_HELUTU
30	58	30.7	546	1	CALX_SOYEN
31	55.5	29.4	611	1	CALG_MOUSE
32	54	28.6	530	1	CALX_ARATH
33	54	28.6	610	1	CALG_HUMAN

34 54 28.6 619 1 CALX_CAEEL
35 51.5 27.2 463 1 VOHA_CHICK
36 51 27.0 725 1 NCA2_MOUSE
37 51 27.0 761 1 NCA2_HUMAN
38 51 27.0 848 1 NCA1_HUMAN
39 51 27.0 853 1 NCA1_BOVIN
40 51 27.0 858 1 NCA1_RAT
41 51 27.0 1091 1 NCA1_CHICK
42 51 27.0 1115 1 NCA1_MOUSE
43 50.5 26.7 236 1 VC05_SPVKA
44 50.5 26.7 560 1 CALX_SCHPO
45 50 26.5 1022 1 DP05_YEAST

ALIGNMENTS

RESULT 1
CRTC_MOUSE
ID CRTC_MOUSE STANDARD; PRT; 416 AA.
AC P14211;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE CALRETICULIN PRECURSOR (CRP55) (CALREGULIN) (HACBP) (ERP60).
GN CALR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 18-48 AND 129-161.
RX STRAIN=BALB/C; TISSUE=Liver;
RX MEDLINE=90059955; PubMed=2583110;
RA Smith M.J., Koch G.L.E.;
RT "Multiple zones in the sequence of calreticulin (CRP55, calregulin, HACBP), a major calcium binding ER/SR protein.";
RL EMBO J. 8:3581-3586(1989).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=93010307; PubMed=1398135;
RA Mazzarella R.A., Gold P., Cunningham M., Green M.;
RT "Determination of the sequence of an expressible cDNA clone encoding ERp60/calregulin by the use of a novel nested set method.";
Gene 120:217-225(1992).
RN [3]
RP SEQUENCE OF 18-38;
RC TISSUE=Fibroblast;
RX MEDLINE=95009907; PubMed=7523108;
RA Merrick B.A., Patterson R.M., Wichter L.L., He C., Selkirk J.K.;
RT "Separation and sequencing of familial and novel murine proteins using preparative two-dimensional gel electrophoresis.";
Electrophoresis 15:735-745(1994).
RL
CC -!- FUNCTION: THIS PROTEIN BINDS CALCIUM. THERE ARE BOTH HIGH AND LOW AFFINITY CALCIUM-BINDING SITES.
CC -!- SUBUNIT: MONOMER (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM LUMEN.
CC -!- SIMILARITY: BELONGS TO THE CALRETICULIN FAMILY.
CC
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CC
CC EMBL; X14926; CAA33053.1;
CC EMBL; M92988; AAA37569.1;
DR PIR; S06763; S06763.
DR PIR; JCL444; JCL444.
DR SWISS-2DPAGE; P14211; MOUSE.
DR MGI; MGI:88252; Calr.

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DR InterPro; IPR001580; Calreticulin.
DR Pfam; PF00262; calreticulin; 1.
DR PRINTS; PR00626; CALRETICULIN.
DR PROSITE; PS001866; Calreticulin; 1.
DR PROSITE; PS00014; ER-TARGET; 1.
DR PROSITE; PS00803; CALRETICULIN_1; 1.
DR PROSITE; PS00804; CALRETICULIN_2; 1.
DR PROSITE; PS00805; CALRETICULIN_REPEAT; 3.
KW Endoplasmic reticulum; Calcium-binding; Repeat; Signal.
FT SIGNAL 1 17
FT CHAIN 18 416 CALRETICULIN.
FT DOMAIN 18 197 N-DOMAIN.
FT DOMAIN 198 308 P-DOMAIN.
FT DOMAIN 309 416 C-DOMAIN.
FT DOMAIN 191 255 4 X APPROXIMATE REPEATS.
FT REPEAT 191 202 1-1.
FT REPEAT 210 221 1-2.
FT REPEAT 227 238 1-3.
FT REPEAT 244 255 1-4.
FT DOMAIN 259 297 3 X APPROXIMATE REPEATS.
FT REPEAT 259 269 2-1.
FT REPEAT 273 283 2-2.
FT REPEAT 287 297 2-3.
FT DOMAIN 351 407 ASP/GLU/LYS-RICH.
FT DISULFID 137 163 BY SIMILARITY.
FT SITE 413 416 PREVENT SECRETION FROM ER.
SQ SEQUENCE 416 AA; 47994 MW; 24C03B00913408D8 CRC64;

Query Match 100.0%; Score 189; DB 1; Length 416;
Best Local Similarity 100.0%; Pred. No. 3.4e-19;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VFVNYGKNVLYNKIDRCDDPETHLYTLVIRPDN 35
    |||||
DB 146 VFVNYGKNVLYNKIDRCDDPETHLYTLVIRPDN 180

RESULT 2
CRTC_RAT
ID CRTC_RAT STANDARD; PRT; 416 AA.
AC P18418; P10452;
DT 01-MAR-1989 (Rel. 10, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE CALRETICULIN PRECURSOR (CRP55) (CALREGULIN) (HACBP) (ERP60) (CALBP)
DE (CALCIUM-BINDING PROTEIN 3) (CABP3).
GN CALR.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID 10116;
PI [1]
SEQUENCE FROM N.A.
RC STRAIN SPRAGUE-DAWLEY; TISSUE Brain cortex;
RX MEDLINE 90370496; PubMed 2395661;
RA Murthy K.K., Banville D., Srikant C.B., Carrier F., Bell A.,
Holmes C., Patel Y.C.;
RT "Structural homology between the rat calreticulin gene product and
the Onchocerca volvulus antigen Ra1-1.";
RL Nucleic Acids Res. 18:4933-4933(1990).
RN [2]
SEQUENCE FROM N.A.
RC STRAIN SPRAGUE-DAWLEY;
RX MEDLINE 93202172; PubMed 8453984;
RA Nakamura M., Moriya M., Baba T., Michikawa Y., Yamanobe T., Arai K.,
Okimura S., Kobayashi T.;
RT "An endoplasmic reticulum protein, calreticulin, is transported into
the acrosome of rat sperm.";
RL exp. Cell Res. 205:101-110(1993).
RN [3]
SEQUENCE FROM N.A.
RC STRAIN SPRAGUE-DAWLEY; TISSUE Liver;
RX MEDLINE 95181573; PubMed-7876339;
RA Soenichsen B., Fuelekruug J., van Nguyen P., Diekmann W.,
Robinson D.G., Mieskes G.;
RT "Retention and retrieval: both mechanisms cooperate to maintain
calreticulin in the endoplasmic reticulum.";
RL J. Cell Sci. 107:2705-2717(1994).
RN [4]
SEQUENCE OF 270-358 FROM N.A.
RC STRAIN-SPRAGUE-DAWLEY;
RA Lone Y.C., Bailly A., Latruffe N.;
RL Submitted (DEC-1988) to the EMBL/GenBank/DBJ databases.
RN [5]
SEQUENCE OF 18-29.
RX MEDLINE-91054414; PubMed-2241926;
RA Treves S., de Mattei M., Lanfredi M., Villa A., Green N.M.,
MacLennan D.H., Meldolesi J., Pozzan T.;
RT "Calreticulin is a candidate for a calsequestrin-like function in
Ca2(+)-storage compartments (calciosomes) of liver and brain.";
RL Biochem. J. 271:473-480(1990).
RN [6]
SEQUENCE OF 18-32.
RC STRAIN SPRAGUE-DAWLEY; TISSUE Testis;
RX MEDLINE-92360010; PubMed-1497655;
RA Nakamura M., Michikawa Y., Baba T., Okinaga S., Arai K.;
RT "Calreticulin is present in the acrosome of spermatids of rat
testis.";
RL Biochem. Biophys. Res. Commun. 186:668-673(1992).
RN [7]
SEQUENCE OF 18-32.
RC STRAIN LEC; TISSUE Liver;
RX MEDLINE-94072621; PubMed-8251535;
RA Yokoi T., Nagayama S., Kajiwara R., Kawaguchi Y., Horiuchi R.,
Kamatani T.;
RT "Identification of protein disulfide isomerase and calreticulin as
autoimmune antigens in LEC strain of rats.";
RL Biochim. Biophys. Acta 1158:339-344(1993).
CC -!- FUNCTION: THIS PROTEIN BINDS CALCIUM. THERE ARE BOTH HIGH AND
LOW AFFINITY CALCIUM-BINDING SITES.
CC -!- SUBUNIT: MONOMER (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM LUMEN.
CC -!- SIMILARITY: BELONGS TO THE CALRETICULIN FAMILY.
CC -!- CAUTION: WAS ORIGINALLY (REF.2) THOUGHT TO BE D-BETA-
HYDROXYBUTYRATE DEHYDROGENASE.
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EMBL; D78308; BAA11345.1; -
DR EMBL; X53363; CAA37446.1; -
DR EMBL; X13702; CAA31987.1; ALT_SEQ.
DR EMBL; X79327; CAA55890.1; -
DR PIR; S04867; S04867.
DR PIR; S11205; S11205.
DR PIR; S13045; S13045.
DR PIR; A49176; A49176.
DR PIR; S45036; S45036.
DR PIR; JH0819; JH0819.
DR InterPro; IPR001580; Calreticulin.
DR InterPro; IPR000886; ER_target.
DR Pfam; PF00262; calreticulin; 1.
DR PRINTS; PR00626; CALRETICULIN.
DR PROSITE; PS001866; Calreticulin; 1.
DR PROSITE; PS00014; ER-TARGET; 1.
DR PROSITE; PS00803; CALRETICULIN_1; 1.
DR PROSITE; PS00804; CALRETICULIN_2; 1.
DR PROSITE; PS00805; CALRETICULIN_REPEAT; 3.
KW Endoplasmic reticulum; Calcium-binding; Repeat; Signal.
KW

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FT SIGNAL 1 17
 FT CHAIN 18 416
 FT DOMAIN 18 197
 FT DOMAIN 18 197
 FT DOMAIN 198 308
 FT DOMAIN 309 416
 FT DOMAIN 191 255
 FT DOMAIN 191 255
 FT REPEAT 191 202
 FT REPEAT 210 221
 FT REPEAT 227 238
 FT REPEAT 244 255
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 FT REPEAT 273 283
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 FT DISULFID 137 163
 FT SITE 413 416
 SQ SEQUENCE.. 416 AA; 47995 MW; 2E6713CED31A2970 CRC64;

Query Match 100.0%; Score 189; DB 1; Length 416;
 Best Local Similarity 100.0%; Pred. No. 3.4e-19;
 Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VFVNYGKNVINKIRCKDDETHLYTLIVRPN 35
 DB 146 VFVNYGKNVINKIRCKDDETHLYTLIVRPN 180

RESULT 3
 CRTCL_HUMAN
 ID CRTCL_HUMAN STANDARD; PRT; 417 AA.
 AC P27797;
 DT 01-AUG-1992 (Rel. 23, Created)
 DT 01-AUG-1992 (Rel. 23, Last sequence update)
 DT 20-AUG-2001 (Rel. 40, Last annotation update)
 DE CALRETICULIN PRECURSOR (CRP55) (CALREGULIN) (HACBP) (ERP60) (52 KDA
 DE RIBONUCLEOPROTEIN AUTOANTIGEN RO/SS-A).
 GN CALR OR CRTCL.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_Taxid:9606;
 RN [1]
 RN SEQUENCE FROM N.A.
 RP MEDLINE=92013129; PubMed=1919005;
 RA Rokeach L.A., Haselby J.A., Melloy J.F., Smeenk R.J., Unnasch T.R.,
 RA Greene B.M., Hoch S.O.;
 RT "Characterization of the autoantigen calreticulin.";
 RL J. Immunol. 147:3031-3039(1991).
 RN [2]
 RN SEQUENCE FROM N.A.
 RP MEDLINE=90237213; PubMed=2332496;
 RA McCaulliffe D.P., Lux F.A., Lieu T.S., Sanz I., Hanke J., Newkirk M.M.,
 RA Bachinski L.L., Itoh Y., Siciliano M.J., Reichlin M., Sontheimer R.D.,
 RA Capra J.D.;
 RT "Molecular cloning, expression, and chromosome 19 localization of a
 RT human Ro/SS-A autoantigen";
 RL J. Clin. Invest. 85:1379-1391(1990).
 RN [3]
 RN SEQUENCE FROM N.A.
 RP MEDLINE=92129342; PubMed=1733953;
 RA McCaulliffe D.P., Yang Y.S., Wilson J., Sontheimer R.D., Capra J.D.;
 RT "The 5'-flanking region of the human calreticulin gene shares
 RT homology with the human GRP78, GRP94, and protein disulfide isomerase
 RT promoters";
 RL J. Biol. Chem. 267:2557-2562(1992).
 RN [4]
 RN SEQUENCE FROM N.A.
 RP Lamerdin J., McCreedy P., Stilwagen S., Ramirez M., Carrano A.;
 RL Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RN SEQUENCE OF 18-36.

RX MEDLINE=92002034; PubMed=1911778;
 RA Rojiani M.V., Finlay B.B., Gray V., Dedhar S.;
 RT "In vitro interaction of a polypeptide homologous to human Ro/SS-A
 RT antigen (calreticulin) with a highly conserved amino acid sequence in
 RT the cytoplasmic domain of integrin alpha subunits.";
 RL Biochemistry 30:9859-9866(1991).
 RN [6]
 RN SEQUENCE OF 18-32.
 RP MEDLINE=90380058; PubMed=2400400;
 RA Krause K.H., Simmerman H.K.B., Jones L.R., Campbell K.P.;
 RT "Sequence similarity of calreticulin with a Ca2(+)-binding protein
 RT that co-purifies with an Ins(1,4,5)P3-sensitive Ca2+ store in HL-60
 RT cells.";
 RL Biochem. J. 270:545-548(1990).
 RN [7]
 RN SEQUENCE OF 18-28.
 RP TISSUE=Liver;
 RC MEDLINE=93162045; PubMed=1286669;
 RX Hochstrasser D.F., Frutiger S., Paquet N., Bairoch A., Ravier F.,
 RA Pasquali C., Sanchez J.-C., Tissot J.-D., Bjellqvist B., Vargas R.,
 RA Appel R.D., Hughes G.J.;
 RT "Human liver protein map: a reference database established by
 RT microsequencing and gel comparison.";
 RL Electrophoresis 13:982-1001(1992).
 RN [8]
 RN PARTIAL SEQUENCE OF 25-34; 56-62; 208-221 AND 273-278.
 RP TISSUE=Keratinocytes;
 RC MEDLINE=93162043; PubMed=1286667;
 RX Rasmussen H.H., van Damme J., Puype M., Gesser B., Celis J.E.,
 RA Vandekerckhove J.;
 RT "Microsequences of 145 proteins recorded in the two-dimensional gel
 RT protein database of normal human epidermal keratinocytes.";
 RL Electrophoresis 13:960-969(1992).
 RN [9]
 RN SEQUENCE OF 18-26.
 RP TISSUE=Colon carcinoma;
 RC MEDLINE=97295306; PubMed=9150948;
 RX Ji H., Reid G.E., Moritz R.L., Eddes J.S., Burgess A.W., Simpson R.J.;
 RA "A two-dimensional gel database of human colon carcinoma proteins.";
 RL Electrophoresis 18:605-613(1997).
 CC 1- FUNCTION: THIS PROTEIN BINDS CALCIUM. THERE ARE BOTH HIGH AND
 CC LOW AFFINITY CALCIUM-BINDING SITES.
 CC 1- SUBUNIT: MONOMER (BY SIMILARITY).
 CC 1- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM LUMEN.
 CC 1- SIMILARITY: BELONGS TO THE CALRETICULIN FAMILY.
 CC 1- CAUTION: WAS ORIGINALLY (REF.2) THOUGHT TO BE THE RO AUTOANTIGEN.
 CC
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 DR EMBL; M84739; AAA51916.1; -
 DR EMBL; M32294; AAA36582.1; -
 DR EMBL; AD000092; AAB51176.1; -
 DR PIR; A37047; A37047.
 DR PIR; S11475; S11475.
 DR PIR; A42330; A42330.
 DR PIR; A46452; A46452.
 DR SWISS-2DPAGE; P27797; HUMAN.
 DR Aarhus/Shent-2DPAGE; 9401; IEF.
 DR HSC-2DPAGE; P27797; HUMAN.
 DR MIM; 109091; -
 DR InterPro; IPR001580; Calreticulin.
 DR InterPro; IPR000886; ER target.
 DR Pfam; PF00262; calreticulin_1.
 DR PRINTS; PR00626; CALRETICULIN.
 DR ProDom; PD001866; Calreticulin; 1.
 DR PROSITE; PS00014; ER-TARGET; 1.
 DR PROSITE; PS00803; CALRETICULIN_1; 1.

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DR PROSITE; PS00804; CALRETICULIN_2; 1.
DR PROSITE; PS00805; CALRETICULIN_REPEAT; 3.
KW Endoplasmic reticulum; Calcium-binding; Repeat; Signal.
FT SIGNAL 1 17
FT CHAIN 18 417 CALRETICULIN.
FT DOMAIN 18 197 N-DOMAIN.
FT DOMAIN 198 308 P-DOMAIN.
FT DOMAIN 309 417 C-DOMAIN.
FT DOMAIN 191 255 4 X APPROXIMATE REPEATS.
FT REPEAT 191 202 1-1.
FT REPEAT 210 221 1-2.
FT REPEAT 227 238 1-3.
FT REPEAT 244 255 1-4.
FT DOMAIN 259 297 3 X APPROXIMATE REPEATS.
FT REPEAT 259 269 2-1.
FT REPEAT 273 283 2-2.
FT REPEAT 287 297 2-3.
FT DOMAIN 351 408 ASP/GLU/LYS-RICH.
FT DISULFID 137 163 BY SIMILARITY.
FT SITE 414 417 PREVENT SECRETION FROM ER.
FT CONFLICT 35 35 MISSING (IN REF. 3).
SQ SEQUENCE 417 AA; 48141 MW; HC37C3C0F1054FB2 CRC64;

Query Match 100.0%; Score 189; DB 1; Length 417;
Best Local Similarity 100.0%; Pred. No. 3.4e-19;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VIPNYGKNVLINKIRCKDDEFTHTLVIRPDN 35
DD 146 VIPNYGKNVLINKIRCKDDEFTHTLVIRPDN 180
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RESULT 4
ID CRTC_RABIT STANDARD; PRT; 418 AA.
AC P15253;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE CALRETICULIN PRECURSOR (CRP55) (CALREGULIN) (HACBP) (ERP60).
GN CALR.
OS Erythrocytes cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID:9986;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-slow-twitch skeletal muscle;
RX MEDLINE 90094320; PubMed 2600080;
RA Fliegel L., Burns K., MacLennan D.H., Reithmeier R.A.F., Michalak M.;
RT "Molecular cloning of the high affinity calcium-binding protein
RT (calreticulin) of skeletal muscle sarcoplasmic reticulum.";
RG J. Biol. Chem. 264:21522-21528(1989).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE Fast-twitch skeletal muscle;
RX MEDLINE 91282795; PubMed 2059224;
RA Fliegel L., Michalak M.;
RT "Fast-twitch and slow-twitch skeletal muscles express the same
RT isoform of calreticulin.";
RL Biochem. Biophys. Res. Commun. 177:979-984(1991).
RN [3]
RP SEQUENCE OF 18-36.
RX MEDLINE 91054414; PubMed 2241926;
RA Treves S., de Mattei M., Lanfretti M., Villa A., Green N.M.;
RA MacLennan D.H., Meldolesi J., Pozzan T.;
RT "Calreticulin is a candidate for a calsequestrin-like function in
RT Ca2(+)-storage compartments (calciosomes) of liver and brain.";
RL Biochem. J. 271:473-480(1990).
RN [4]
RP SEQUENCE OF 18-46.
RX MEDLINE 91201375; PubMed 2016321;

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RA Milner R.E., Baksh S., Shemanko C., Carpenter M.R., Smillie L.,
RA Vance J.E., Opas M., Michalak M.;
RT "Calreticulin, and not calsequestrin, is the major calcium binding
RT protein of smooth muscle sarcoplasmic reticulum and liver endoplasmic
RT reticulum.";
RL J. Biol. Chem. 266:7155-7165(1991).
RN [5]
RP PARTIAL SEQUENCE.
RC TISSUE=Lung;
RX MEDLINE 92002038; PubMed 1911780;
RA Guan S., Falick A.M., Williams D.E., Cashman J.R.;
RT "Evidence for complex formation between rabbit lung flavin-containing
RT monooxygenase and calreticulin.";
RL Biochemistry 30:9892-9900(1991).
CC -!- FUNCTION: THIS PROTEIN BINDS CALCIUM. THERE ARE BOTH HIGH AND
CC -!- LOW AFFINITY CALCIUM-BINDING SITES.
CC -!- SUBUNIT: MONOMER (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM LUMEN.
CC -!- SIMILARITY: BELONGS TO THE CALRETICULIN FAMILY.
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CC -----
DR EMBL; J05138; AAA31188.1; -
DR PIR; A34154; A34154.
DR PIR; C33208; C33208.
DR PIR; D33208; D33208.
DR PIR; E33208; E33208.
DR PIR; F33208; F33208.
DR PIR; S13046; S13046.
DR PIR; S13047; S13047.
DR InterPro; IPR001580; Calreticulin.
DR InterPro; IPR000886; ER_target.
DR Pfam; PF00262; calreticulin; 1.
DR PRINTS; PR00626; CALRETICULIN.
DR ProDom; PD001866; Calreticulin; 1.
DR PROSITE; PS00014; ER_TARGET; 1.
DR PROSITE; PS00803; CALRETICULIN_1; 1.
DR PROSITE; PS00804; CALRETICULIN_2; 1.
DR PROSITE; PS00805; CALRETICULIN_REPEAT; 3.
KW Endoplasmic reticulum; Calcium-binding; Repeat; Signal.
FT SIGNAL 1 17
FT CHAIN 18 418 CALRETICULIN.
FT DOMAIN 18 197 N-DOMAIN.
FT DOMAIN 198 308 P-DOMAIN.
FT DOMAIN 309 418 C-DOMAIN.
FT DOMAIN 191 255 4 X APPROXIMATE REPEATS.
FT REPEAT 191 202 1-1.
FT REPEAT 210 221 1-2.
FT REPEAT 227 238 1-3.
FT REPEAT 244 255 1-4.
FT DOMAIN 259 297 3 X APPROXIMATE REPEATS.
FT REPEAT 259 269 2-1.
FT REPEAT 273 283 2-2.
FT REPEAT 287 297 2-3.
FT DOMAIN 351 408 ASP/GLU/LYS-RICH.
FT DISULFID 137 163 BY SIMILARITY.
FT SITE 415 418 PREVENT SECRETION FROM ER.
FT VARIANT 35 35 E -> D.
FT CONFLICT 90 90 P -> T (IN REF. 5).
SQ SEQUENCE 418 AA; 48275 MW; B6082B689DC763A6 CRC64;

Query Match 100.0%; Score 189; DB 1; Length 418;
Best Local Similarity 100.0%; Pred. No. 3.4e-19;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VIPNYGKNVLINKIRCKDDEFTHTLVIRPDN 35

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Db 146 VIFNYGKGNVLINKDIRCKDDEFTHTLVLRPN 180
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RESULT 5
CRTL_BOVIN
ID CRTL_BOVIN STANDARD: PRT: 400 AA.
AC P52193;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE CALRETICULIN, BRAIN ISOFORM 1 (CRP55) (CALREGULIN) (HACBP).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE.
RC TISSUE=Brain;
RX MEDLINE=94183174; PubMed=8135753;
RA Matsuoka K., Seta K., Yamakawa Y., Okuyama T., Shinoda T., Isobe T.;
RT "Covalent structure of bovine brain calreticulin.";
RL Biochem. J. 298:435-442(1994).
CC -!- FUNCTION: THIS PROTEIN BINDS CALCIUM. THERE ARE BOTH HIGH AND
CC LOW AFFINITY CALCIUM-BINDING SITES.
CC -!- SUBUNIT: MONOMER.
CC -!- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM LUMEN.
CC -!- SIMILARITY: BELONGS TO THE CALRETICULIN FAMILY.
DR InterPro; IPR001580; Calreticulin.
DR Pfam; PF00262; calreticulin; 1.
DR ProDom; PD001866; Calreticulin.
DR PRINTS; PR00626; CALRETICULIN.
DR PROSITE; PS00014; ER_TARGET; 1.
DR PROSITE; PS00803; CALRETICULIN_1; 1.
DR PROSITE; PS00804; CALRETICULIN_2; 1.
DR PROSITE; PS00805; CALRETICULIN_REPEAT; 3.
KW Endoplasmic reticulum; Calcium-binding; Repeat; Glycoprotein.
FT DOMAIN 1 180
FT DOMAIN 181 291
FT DOMAIN 292 400
FT DOMAIN 401 511
FT REPEAT 174 238
FT REPEAT 174 185
FT REPEAT 193 204
FT REPEAT 210 221
FT REPEAT 227 238
FT REPEAT 242 280
FT REPEAT 242 252
FT REPEAT 256 266
FT REPEAT 270 280
FT REPEAT 280 280
FT DOMAIN 334 390
FT DOMAIN 390 416
FT DISULFID 120 162
FT CARBOHYD 162 162
FT SITE 397 400
SQ SEQUENCE 400 AA; 46381 MW; 7D486BDFC689EEF1 CRC64;

Query Match 97.4%; Score 184; DB 1; Length 400;
Best Local Similarity 97.1%; Pred. No. 1.6e-18;
Matches 34; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VIFNYGKGNVLINKDIRCKDDEFTHTLVLRPN 35
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Db 129 VIFNYGKGNVLINKDIRCKDDEFTHTLVLRPN 163
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RESULT 6
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ID CRTL_BOVIN STANDARD: PRT: 421 AA.
AC P42918;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)

15-JUL-1998 (Rel. 36, Last annotation update)
DE CALRETICULIN, BRAIN ISOFORM 2 PRECURSOR (CRP55) (CALREGULIN) (HACBP).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=93385184; PubMed=8373827;
RA Liu N., Fine R.E., Johnson R.J.;
RT "Comparison of cDNAs from bovine brain coding for two isoforms of
calreticulin.";
RL Biochim. Biophys. Acta 1202:70-76(1993).
CC -!- FUNCTION: THIS PROTEIN BINDS CALCIUM. THERE ARE BOTH HIGH AND
CC LOW AFFINITY CALCIUM-BINDING SITES.
CC -!- SUBUNIT: MONOMER (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM LUMEN.
CC -!- SIMILARITY: BELONGS TO THE CALRETICULIN FAMILY.
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CC -----
EMBL; L13462; AAC37307.1;
DR InterPro; IPR001580; Calreticulin.
DR Pfam; PF00262; calreticulin; 1.
DR PRINTS; PR00626; CALRETICULIN.
DR ProDom; PD001866; Calreticulin; 1.
DR PROSITE; PS00014; ER_TARGET; 1.
DR PROSITE; PS00803; CALRETICULIN_1; 1.
DR PROSITE; PS00804; CALRETICULIN_2; 1.
DR PROSITE; PS00805; CALRETICULIN_REPEAT; 3.
KW Endoplasmic reticulum; Calcium-binding; Repeat; Signal.
FT SIGNAL 1 34
FT CHAIN 35 421
FT DOMAIN 35 201
FT DOMAIN 202 312
FT DOMAIN 313 421
FT DOMAIN 195 259
FT REPEAT 195 206
FT REPEAT 214 225
FT REPEAT 231 242
FT REPEAT 248 259
FT DOMAIN 263 301
FT REPEAT 263 273
FT REPEAT 277 287
FT REPEAT 291 301
FT DOMAIN 366 411
FT DISULFID 141 167
FT CARBOHYD 183 183
FT SITE 418 421
SQ SEQUENCE 421 AA; 48812 MW; 0257E959F71528BC CRC64;

Query Match 97.4%; Score 184; DB 1; Length 421;
Best Local Similarity 97.1%; Pred. No. 1.7e-18;
Matches 34; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VIFNYGKGNVLINKDIRCKDDEFTHTLVLRPN 35
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Db 150 VIFNYGKGNVLINKDIRCKDDEFTHTLVLRPN 184
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RESULT 7
CRTL_DROME
ID CRTL_DROME STANDARD: PRT: 406 AA.
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AC P29413; Q9VHA3;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-OCT-1993 (Rel. 27, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE CALRETICULIN PRECURSOR (CRP55) (CALREGULIN) (HACBP).
GN CRC OR CG9429.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Aphidrodidae; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93208374; PubMed.1396819;
RA Smith M.J.;
RT "Nucleotide sequence of a Drosophila melanogaster gene encoding a
  calreticulin homologue."
RL DNA Seq. 3:247-250(1992).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN BERKELEY.
RX MEDLINE 20196006; PubMed:10731132;
RA Adams M.D., Gailinker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.C., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Vandeil M.D., Zhang Q., Chen L.X.,
RA Brannon R.C., Rogers J.H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Holt G., Nelson C.R., Miklos G.L.G.,
RA Brill J.F., Agbayani A., An H.-J., Andrews-Frankoch C., Baldwin D.,
RA Ballou R.M., Basu A., Buxendell J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokatein P., Brothier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablo S., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evansgill C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Foaier C., Gabrielian A.E., Garq N.S., Gelbart W.M., Glasser K.,
RA Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Mei M.-H., Ibegwam C.,
RA Julali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lanko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Morkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nilsson D.R., Nilsson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue H.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Sprudling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissensbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs K.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster."
RL Science 287:2185-2195(2000).
RN [3]
RP SEQUENCE OF 91-124 AND 182-220.
RX MEDLINE 90307981; PubMed.2365822;
RA McCaulliff D.P., Zuppi E., Lieu T.S., Michalak M., Sontheimer R.D.,
RA Cupra J.D.;
RT "A human Ro/SS-A autoantigen is the homologue of calreticulin and is
  highly homologous with onchocercal RAL-1 antigen and an aplasia
  'memory molecule'."
RL J. Clin. Invest. 86:332-335(1990).
CC -I- FUNCTION: THIS PROTEIN BINDS CALCIUM. THERE ARE BOTH HIGH AND
  LOW AFFINITY CALCIUM-BINDING SITES.
CC -I- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM LUMEN.
CC -I- SIMILARITY: BELONGS TO THE CALRETICULIN FAMILY.

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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X64461; CAA45791.1; -.
DR EMBL; AE003683; AAF34416.1; -.
DR PIR; A37158; A37158.
DR FlyBase; FBgn005585; Crc.
DR InterPro; IPR001580; Calreticulin.
DR InterPro; IPR000886; ER_target.
DR Pfam; PF00262; calreticulin; 1.
DR PRINTS; PR00626; CALRETICULIN.
DR ProDom; PD001866; Calreticulin; 1.
DR PROSITE; PS00014; ER_TARGET; 1.
DR PROSITE; PS00803; CALRETICULIN_1; 1.
DR PROSITE; PS00804; CALRETICULIN_2; 1.
DR PROSITE; PS00805; CALRETICULIN_REPEAT; 3.
DR Endoplasmic reticulum; Calcium-binding; Repeat; Signal.
FT SIGNAL 1 17 POTENTIAL.
FT CHAIN 18 406 CALRETICULIN.
FT CONFLICT 107 107 G -> A (IN REF. 3).
FT CONFLICT 184 184 V -> L (IN REF. 3).
SQ SEQUENCE 406 AA; 46808 MW; 65D72C69D0BEC427 CRC64;

Query Match 83.6%; Score 158; DB 1; Length 406;
Best Local Similarity 82.9%; Pred. No. 7.6e-15;
Matches 29; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 VFNFKGNKLVINKDIRCKDDETHLYTLIVRPDN 35
Db 146 VFNFKGNKLVINKDIRCKDDETHLYTLIVRPDN 180
|||||
146 VFNFKGNKLVINKDIRCKDDETHLYTLIVRPDN 180
|||||

RESULT 8
RALL_ONCVO STANDARD; PRT; 388 AA.
AC P11012;
DT 01-JUL-1989 (Rel. 11, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE RAL-1 PROTEIN PRECURSOR (41 KDA LARVAL ANTIGEN).
GN RALI.
OS Onchocerca volvulus.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea;
OC Onchocercidae; Onchocerca.
OX NCBI_TaxID=6282;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94341871; PubMed=7520419;
RA Rokeach L.A., Zimmerman P.A., Unnasch T.R.;
RT "Epitopes of the Onchocerca volvulus RAL1 antigen, a member of the
  calreticulin family of proteins, recognized by sera from patients
  with onchocerciasis."
RL Infect. Immun. 62:3696-3704(1994).
RN [2]
RP SEQUENCE OF 53-388 FROM N.A.
RX MEDLINE=8273584; PubMed=2455736;
RA Unnasch T.R., Gallin M.Y., Soboslay P.T., Erttmann K.D., Greene B.M.;
RT "Isolation and characterization of expression cDNA clones encoding
  antigens of Onchocerca volvulus infective larvae."
RL J. Clin. Invest. 82:262-269(1988).
CC -I- SIMILARITY: BELONGS TO THE CALRETICULIN FAMILY.
CC -----
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CC EMBL; M20565; AAA59056.1; -
CC PIR; A32507; A32507.
CC InterPro; IPR001580; Calreticulin.
CC Pfam; PF00262; calreticulin; 1.
CC PRINTS; P00626; CALRETICULIN.
CC PRODOM; PD001866; Calreticulin; 1.
CC PROSITE; PS00803; CALRETICULIN_1; 1.
CC PROSITE; PS00804; CALRETICULIN_2; 1.
CC PROSITE; PS00805; CALRETICULIN_REPEAT; 3.
KW Calcium-binding; Repeat; Antigen; Signal.
FT SIGNAL 1 17 POTENTIAL.
FT CHAIN 18 353 RAL-1 PROTEIN.
FT DOMAIN 189 253 4 X APPROXIMATE REPEATS.
FT REPEAT 189 200 1-1.
FT REPEAT 208 219 1-2.
FT REPEAT 225 236 1-3.
FT REPEAT 242 253 1-4.
FT DOMAIN 257 295 3 X APPROXIMATE REPEATS.
FT REPEAT 257 267 2-1.
FT REPEAT 271 281 2-2.
FT REPEAT 285 295 2-3.
FT DOMAIN 353 388 ARG/LYS-RICH (BASIC).
FT DISULFID 135 161 BY SIMILARITY.
SQ SEQUENCE 388 AA; 45298 MW; 9537F298A2D31CD6 CRC64;

Query Match 73.5%; Score 139; DB 1; Length 388;
Best Local Similarity 74.3%; Pred. No. 3.4e-12;
Matches 26; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 1 VIFNKGKLVNLIKDKCKDDEFTHLYTLIVRPDN 35
   |||||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
DB 144 VIFKDRNRHMIKKDKCKDDVFTHLYTLIVNSDN 178

RESULT 9
CRTC_SCHMA
ID CRTC_SCHMA STANDARD; PRT; 393 AA.
AC Q06814; Q26562;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE CALRETICULIN PRECURSOR (SM4 PROTEIN).
OS Schistosoma mansoni (Blood fluke).
OC Eukaryota; Metazoa; Platyhelminthes; Turbellarian Platyhelminths;
OC Rhabditophora; Eulcithophora; Revertospermata; Mediofusata;
OC Neodermata; Trematoda; Digenea; Strigeidida; Schistosomatoidea;
OC Schistosomatidae; Schistosoma.
OX NCBI_TaxID=6183;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PUERTO RICAN;
RX MEDLINE=93165070; PubMed=8433712;
RA Khalife J., Trottein F., Schacht A.-M., Godin C., Pierce R.J.,
RA Capron A.;
RT "Cloning of the gene encoding a Schistosoma mansoni antigen
RT homologous to human Ro/SS-A autoantigen.";
RL Mol. Biochem. Parasitol. 57:193-202(1993).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=PUERTO RICAN;
RX MEDLINE=94187805; PubMed=8139623;
RA Khalife J., Pierce R.J., Godin C., Capron A.;
RT "Cloning and sequencing of the gene encoding Schistosoma mansoni
RT calreticulin.";
RL Mol. Biochem. Parasitol. 62:313-315(1993).
CC -!- FUNCTION: THIS PROTEIN BINDS CALCIUM. THERE ARE BOTH HIGH AND
CC -!- LOW AFFINITY CALCIUM-BINDING SITES.
CC -!- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM LUMEN.

-!- SIMILARITY: BELONGS TO THE CALRETICULIN FAMILY.
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CC EMBL; M93097; AAA29854.1; -
CC EMBL; L24159; AAA19024.1; -
CC HSP; P00268; ARXN.
CC InterPro; IPR001580; Calreticulin.
CC InterPro; IPR000886; ER_target.
CC Pfam; PF00262; calreticulin; 1.
CC PRINTS; P00626; CALRETICULIN.
CC PRODOM; PD001866; Calreticulin; 1.
CC PROSITE; PS00803; CALRETICULIN_1; 1.
CC PROSITE; PS00804; CALRETICULIN_2; 1.
CC PROSITE; PS00805; CALRETICULIN_REPEAT; 1.
KW Endoplasmic reticulum; Calcium-binding; Repeat; Signal; Glycoprotein.
FT SIGNAL 1 16 POTENTIAL.
FT CHAIN 17 393 CALRETICULIN.
FT DOMAIN 189 254 4 X 12 AA APPROXIMATE REPEATS.
FT REPEAT 189 200 1-1.
FT REPEAT 209 220 1-2.
FT REPEAT 225 236 1-3.
FT REPEAT 243 254 1-4.
FT DOMAIN 257 295 3 X 11 AA APPROXIMATE REPEATS.
FT REPEAT 257 267 2-1.
FT REPEAT 271 281 2-2.
FT REPEAT 285 295 2-3.
FT CARBOHYD 27 27 N-LINKED (GLCNAC. .) (POTENTIAL).
FT DISULFID 135 161 BY SIMILARITY.
FT SITE 390 393 PREVENT SECRETION FROM ER.
FT CONFLICT 89 90 MV -> IL (IN REF. 2).
FT CONFLICT 188 207 MISSING (IN REF. 2).
FT CONFLICT 378 378 Y -> D (IN REF. 2).
SQ SEQUENCE 393 AA; 45397 MW; 45F59857C21940D2 CRC64;

Query Match 73.0%; Score 138; DB 1; Length 393;
Best Local Similarity 77.1%; Pred. No. 4.8e-12;
Matches 27; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 1 VIFNKGKLVNLIKDKCKDDEFTHLYTLIVRPDN 35
   |||||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
DB 144 VIFNKGKLVNLIKDKCKDDEFTHLYTLIVNPN 178

RESULT 10
CRTC_CAEL
ID CRTC_CAEL STANDARD; PRT; 395 AA.
AC P27798;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 01-FEB-1994 (Rel. 28, Last annotation update)
DE CALRETICULIN PRECURSOR.
GN CRT-1.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditioidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BRISTOL N2;
RX MEDLINE=92329978; PubMed=1627827;
RA Smith M.J.;
RT "A C. elegans gene encodes a protein homologous to mammalian
RT calreticulin.";
RL DNA Seq. 2:235-240(1992).
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DR InterPro: IPR001580; Calreticulin.
DR InterPro: IPR000886; ER_target.
DR Pfam: PF00262; calreticulin; 1.
DR PRINTS: PR00626; CALRETICULIN.
DR ProDom: PD001866; Calreticulin; 1.
DR PROSITE: PS00014; ER_TARGET; 1.
DR PROSITE: PS00803; CALRETICULIN_1; 1.
DR PROSITE: PS00804; CALRETICULIN_2; 1.
DR PROSITE: PS00805; CALRETICULIN_REPEAT; 2.
KW Endoplasmic reticulum; Calcium-binding; Repeat; Signal; Glycoprotein.
FT SIGNAL 1 25 POTENTIAL.
FT CHAIN 26 416 CALRETICULIN.
FT CARBOHYD 57 157 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 157 157 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT SITE 413 416 PREVENT SECRETION FROM ER (POTENTIAL).
SQ SEQUENCE 416 AA; 48136 MW; 565FEC3489F77CA7 CRC64;

Query Match 58.2%; Score 110; DB 1; Length 416;
Best Local Similarity 57.6%; Pred. No. 4.4e-08;
Matches 19; Conservative 5; Mismatches 9; Indels 0; Gaps 0;

QY 2 IFNYDKGNVLINKDKDETHLYTLIVRPD 34
    |||| | ||| : | : | : ||| : |||
DB 153 IFNYDTHLKKDVPCTDQLTHVTLIVRPD 185

RESULT 13
CRTC_DICDI
ID CRTC_DICDI STANDARD; PRT; 424 AA.
AC Q23858;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE CALRETICULIN PRECURSOR.
OS Dictyostelium discoideum (Slime mold).
OC Eukaryota; Mycetozoa; Dictyostellida; Dictyostellium.
OX NCBI_TaxID=44689;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=AX3;
RA Mueller-Taubenberger A., Gerisch G.;
RL Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: THIS PROTEIN BINDS CALCIUM. THERE ARE BOTH HIGH AND
CC LOW AFFINITY CALCIUM-BINDING SITES (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM LUMEN.
CC -!- SIMILARITY: BELONGS TO THE CALRETICULIN FAMILY.
CC
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CC
CC EMBL: U36937; AAB87719.1; -.
CC DictyDB: DD00042; -.
DR InterPro: IPR001580; Calreticulin.
DR InterPro: IPR000886; ER_target.
DR Pfam: PF00262; calreticulin; 1.
DR PRINTS: PR00626; CALRETICULIN.
DR ProDom: PD001866; Calreticulin; 1.
DR PROSITE: PS00804; CALRETICULIN_1; 1.
DR PROSITE: PS00805; CALRETICULIN_2; 1.
DR PROSITE: PS00803; CALRETICULIN_REPEAT; 1.
DR PROSITE: PS00014; ER_TARGET; 1.
KW Endoplasmic reticulum; Calcium-binding; Repeat; Signal.
FT SIGNAL 1 19 POTENTIAL.
FT CHAIN 20 424 CALRETICULIN.
FT DOMAIN 191 257 4 X 12 AA APPROXIMATE REPEATS.
FT REPEAT 191 202 1-1.
FT REPEAT 211 222 1-2.
FT REPEAT 227 238 1-3.

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FT REPEAT 246 257 1-4.
FT DOMAIN 260 298 3 X 11 AA APPROXIMATE REPEATS.
FT REPEAT 260 270 2-1.
FT REPEAT 274 284 2-2.
FT REPEAT 288 298 2-3.
FT DISULFID 105 137 BY SIMILARITY.
FT SITE 421 424 PREVENT SECRETION FROM ER (POTENTIAL).
SQ SEQUENCE 424 AA; 48350 MW; BAF273694FB6FC37 CRC64;

Query Match 57.4%; Score 108.5; DB 1; Length 424;
Best Local Similarity 58.3%; Pred. No. 7.3e-08;
Matches 21; Conservative 6; Mismatches 8; Indels 1; Gaps 1;

QY 1 VIFNYKGNVLINKDI-RCKDDETHLYTLIVRPD 35
    || ||||| ||| : | : | : ||| : |||
DB 145 VILNYKGNHLIKKEINKVETDQLTHVTLIVRPD 180

RESULT 14
CRTC_PRUAR
ID CRTC_PRUAR STANDARD; PRT; 421 AA.
AC Q9XF98;
DT 20-AUG-2001 (Rel. 40, Created)
DT 20-AUG-2001 (Rel. 40, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE CALRETICULIN PRECURSOR.
OS Prunus armeniaca (Apricot).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids I; Rosales; Rosaceae; Prunus.
OX NCBI_TaxID=36596;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. BERGERON; TISSUE=Mesocarp, and Endocarp;
RA Mbeque-A-Mbeque D., Fils-Lycaon B.R.;
RL "Molecular cloning and nucleotide sequence of a calreticulin from
RL apricot (Prunus armeniaca cv. Bergeron).";
RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: THIS PROTEIN BINDS CALCIUM. THERE ARE BOTH HIGH AND
CC LOW AFFINITY CALCIUM-BINDING SITES (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM LUMEN (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE CALRETICULIN FAMILY.
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL: AF134733; AAD32207.1; -.
DR InterPro: IPR001580; Calreticulin.
DR InterPro: IPR000886; ER_target.
DR Pfam: PF00262; calreticulin; 1.
DR PRINTS: PR00626; CALRETICULIN.
DR ProDom: PD001866; Calreticulin; 1.
DR PROSITE: PS00014; ER_TARGET; 1.
DR PROSITE: PS00803; CALRETICULIN_1; 1.
DR PROSITE: PS00804; CALRETICULIN_2; 1.
DR PROSITE: PS00805; CALRETICULIN_REPEAT; 2.
KW Endoplasmic reticulum; Calcium-binding; Repeat; Signal; Glycoprotein.
FT SIGNAL 1 22 POTENTIAL.
FT CHAIN 23 421 CALRETICULIN.
FT CARBOHYD 56 56 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 156 156 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT SITE 418 421 PREVENT SECRETION FROM ER (POTENTIAL).
SQ SEQUENCE 421 AA; 48416 MW; 4F5F94CBAA6C6690 CRC64;

Query Match 56.6%; Score 107; DB 1; Length 421;
Best Local Similarity 54.5%; Pred. No. 1.2e-07;

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Matches 18; Conservative 5; Mismatches 10; Indels 0; Gaps 0;

Qy 2 IFNYKGNVLINKDIRCKDDEFTHLYTLIVRPD 34
152 ILNYNTNLIKDKVPCETDQLTHVYTFIIRPD 184

RESULT 15

CRTC_RICCO	ID	STANDARD;	PRT;	415 AA.
AC	CRTC_RICCO			
AD	P03508;			
DF	20-AUG-2001	(Rel. 40, Created)		
DF	20-AUG-2001	(Rel. 40, Last sequence update)		
DF	20-AUG-2001	(Rel. 40, Last annotation update)		
DE	CALRETTICULIN PRECURSOR.			
OS	Ricinus communis (Castor bean).			
OX:	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;			
OX:	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;			
OX:	eurosid I; Malpighiales; Euphorbiaceae; Ricinus.			
NCBI_TaxID	3988;			
RN	[1]			

RP SEQUENCE FROM N. A.

RX MEDLINE:97435975; Pubmed 9290642;
 NA Coughlan S.J., Hastings C., Winfrey R. Jr.;
 KT "Cloning and characterization of the calreticulin gene from Ricinus
 RT communis L.;
 RL Plant Mol. Biol. 34:897-911(1997).
 CC -1- FUNCTION: THIS PROTEIN BINDS CALCIUM. THERE ARE BOTH HIGH AND
 CC LOW AFFINITY CALCIUM-BINDING SITES.
 CC -1- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM LUMEN.
 CC -1- SIMILARITY: BELONGS TO THE CALRETICULIN FAMILY.
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DR EMRL: U74631: AAB71420.1: -

DR
EMBL: U74630: AAB71419.1: -

DB Mendel: 10452: R1500: 1166-10452

DR
MELNERT; 10432, KICAO; 1108; 10432.
Interpro: 188001580: Call callin is

DK
DB
Interpro: IPR001380; CAZymeCATH;
Interpro: IPR000886; FB tagot

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DK INTCPU; IPR000886; ER_target.
DK Bfam; BW0262; calloutcallin; 1

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DR PLUM; PF00282; calreticulin; I.
PRINTS. PB00626. CAL RETICULIN

DR PRINTS; PRO0626; CALRETICULIN.
DR PRO01955. CALRETICULIN.

BR Prodrom; PB001866; Calreticulin; 1.
BR PROSITR. PB00014. PB PROSITR. 1
BR PROSITR. PB00014. PB PROSITR. 1

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DR PROSITE; PS00014; ER_TARGET; 1.
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DR PROSITE; PS00803; CALRETICULIN_1;
DR PROSITE; PS00804

DR PROSITE; PS00804; CALRETICULIN_2;

DR PROSITE; PS00805; CALRETICULIN_REF

KW Endoplasmic reticulum; Calcium-binding

1 ST SIGNAL	1	20	POTENTIAL
1	1	20	POTENTIAL

F-T	CHAIN	21	415	CALRE
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2	2	2	2	2
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83	83	83	83	83
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85	85	85	85	85
86	86	86	86	86
87	87	87	87	

F ¹ T	CARROHYD	52	52	N-LIN
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F ^T	CARBOHYD	152	152	N-LIN
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SQ SEQUENCE 415 AA; 47522 MW; DD5

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Query Match	Score
1	55.68

Best. local Similarity 51.50: pred.

Matches 17: Conservative

DATE: 11/11/77
PAGE: 11

2 TF'NYKGNVLINKDIRCKDDEETHI.YT.I.

2 1 F N I K R N V E I N K D I K R O D E F I A H I L I L

148 II.NYNDT.NH.I.KKKEVPCE.TDOIT.HVY.T.V.

52 1ENINDINAGLTKREVFCEDQLTHVILV
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Search completed: January 9, 2002, 15:12:16
Job time: 658 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 9, 2002, 15:03:29 ; Search time 78.15 Seconds
(without alignments)
65.509 Million cell updates/sec

Title: US-09-828-000-7
Perfect score: 189
Sequence: 1 VFNKGKVNLINKRCKDDETHLYTLIVRPD 35

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 473505 seqs, 146272329 residues

Total number of hits satisfying chosen parameters: 473505

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- 1: SP_TREMBL_17.*
- 2: sp_archaea.*
- 3: sp_bacteria.*
- 4: sp_fungi.*
- 5: sp_human.*
- 6: sp_invertebrate.*
- 7: sp_mammal.*
- 8: sp_mhc.*
- 9: sp_organelle.*
- 10: sp_phase.*
- 11: sp_plant.*
- 12: sp_rhodent.*
- 13: sp_virus.*
- 14: sp_unclassified.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	173	91.5	318	13 Q9PTX7	Q9ptx7 lampetra re
2	169	89.4	421	5 Q9U6S0	Q9u6s0 strongyloce
3	168	88.9	405	5 Q26268	Q26268 aplysia cal
4	168	88.9	410	5 Q16893	Q16893 amblyomma a
5	161	85.2	343	13 Q91711	Q91711 xenopus lae
6	161	85.2	411	13 Q91710	Q91710 xenopus lae
7	158	83.6	406	5 Q9U916	Q9u916 drosophila
8	154	81.5	417	13 Q9PUC1	Q9pucl brachydanio
9	153	81.0	350	5 Q26514	Q26514 schistosoma
10	153	81.0	396	5 Q45034	Q45034 schistosoma
11	153	81.0	403	5 Q76961	Q76961 necator ame
12	148	78.3	419	13 Q98984	Q98984 rana rugosa
13	146	77.2	375	5 Q18478	Q18478 litomosoid
14	146	77.2	387	5 Q97372	Q97372 difofilaria
15	128	67.7	321	13 Q9U560	Q9u560 eptatretus
16	107	56.6	321	10 Q41799	Q41799 zea mays (m
17	107	56.6	421	10 Q43712	Q43712 zea mays (m
18	104	55.0	412	10 Q40040	Q40040 hordeum vul
19	104	55.0	415	10 Q40041	Q40041 hordeum vul

20	98.5	52.1	427	10 Q9FYV2	Q9fyv2 pinus taeda
21	98	51.9	422	10 Q22502	Q22502 brassica na
22	94	49.7	137	11 Q9D373	Q9d373 mus musculu
23	94	49.7	240	10 Q9ST29	Q9st29 solanum mel
24	94	49.7	380	11 Q9D906	Q9d906 mus musculu
25	94	49.7	389	10 Q40567	Q40567 nicotiana t
26	77	40.7	559	5 Q9NC26	Q9nc26 tritricomo
27	72	38.1	401	5 Q9U9N9	Q9u9n9 trypanosoma
28	72	38.1	403	5 Q9XYF8	Q9xyf8 trypanosoma
29	71	37.6	582	5 Q76214	Q76214 schistosoma
30	71	37.6	582	5 Q9TVF3	Q9tvf3 schistosoma
31	67.5	35.7	872	5 Q26045	Q26045 proliferati
32	66	34.9	397	5 Q94592	Q94592 leishmania
33	66	34.9	582	5 Q04702	Q04702 schistosoma
34	65	34.4	214	4 Q9UDG2	Q9udg2 homo sapien
35	64	33.9	540	2 Q53293	Q53293 acinetobact
36	64	33.9	541	2 Q56752	Q56752 bergeyella
37	63	33.3	291	5 Q9Y1V1	Q9y1v1 leishmania
38	61.5	32.5	455	5 Q9BMP7	Q9bmp7 plasmodium
39	60	31.7	581	5 Q9BLH3	Q9blh3 halocynthia
40	60	31.7	622	13 Q98985	Q98985 rana rugosa
41	59	31.2	543	5 Q9VVP4	Q9vvp4 drosophila
42	59	31.2	545	5 Q9VAL7	Q9val7 drosophila
43	59	31.2	556	5 Q917S9	Q917s9 drosophila
44	59	31.2	583	5 Q9VXF6	Q9vxf6 drosophila
45	59	31.2	605	5 Q02393	Q02393 drosophila

ALIGNMENTS

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RESULT 1
Q9PTX7 PRELIMINARY; PRT; 318 AA.
ID Q9PTX7
AC Q9PTX7
DT 01-MAY-2000 (TRENBLrel. 13, Created)
DE 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DE 01-JUN-2001 (TRENBLrel. 17, Last annotation update)
DE CALRETICULIN (FRAGMENT).
OS Lampetra reissneri.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Hypochoarta;
OC Petromyzontiformes; Petromyzontidae; Lampetra.
OX NCBI_TaxID=7753;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20063780; PubMed=10594174;
RA Kuraku S., Hoshiyama D., Katoh K., Suga H., Miyata T.;
RT "Monophyly of lampreys and hagfishes supported by nuclear DNA-coded
RT genes.";
RL J. Mol. Evol. 49:729-735(1999).
DR EMBL: AB025328; BAA88481.1; -.
DR InterPro: IPR000886; ER_target.
DR InterPro: IPR001580; Calreticulin.
DR Pfam: PF00262; calreticulin; 1.
DR PRINTS: PR00626; CALRETICULIN.
DR ProDom: PD001866; Calreticulin; 1.
DR PROSITE: PS00804; CALRETICULIN_2; 1.
DR PROSITE: PS00805; CALRETICULIN_REPEAT; 3.
DR PROSITE: PS00014; ER_TARGET; UNKNOWN_1.
FT NON_TER 1
SQ SEQUENCE 318 AA; 36997 MW; C88102EA1CAC1506 CRC64;

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Query Match 91.5%; Score 173; DB 13; Length 318;
Best Local Similarity 94.1%; Pred. No. 3.4e-16;
Matches 32; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 VFNKGKVNLINKRCKDDETHLYTLIVRPD 34
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Db 45 VFNKGKVNLINKRCKDDETHLYTLIVRPD 78
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RESULT 2

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Q9U6S0
ID Q9U6S0 PRELIMINARY; PRT; 421 AA.
AC Q9U6S0
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE CALRETICULIN PRECURSOR.
GN CALRT.
OS Strongylocentrotus purpuratus (Purple sea urchin).
OC Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
OC Rhinzoidea; Euechinozoa; Echinacea; Echinoida; Strongylocentrotidae;
OC Strongylocentrotus.
OX NCBI_TaxID 7668;
RN [1]
RP SEQUENCE FROM N.A.
KA Susan J.M., Just M.L., Lennarz W.J.;
KT "Cloning and Characterization of AlphaP Integrin and Calreticulin in
RT Embryos of the Sea Urchin.";
RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF177915; RAD55725.1; -
DR InterPro; IPR000886; ER_target.
DR InterPro; IPR001580; Calreticulin.
DR Pfam; PF00262; calreticulin; 1.
DR PRINTS; PR00626; CALRETICULIN.
DR ProDom; PD001866; Calreticulin; 1.
DR PROSITE; PS00804; CALRETICULIN_2; 1.
DR PROSITE; PS00805; CALRETICULIN_REPEAT; 3.
DR PROSITE; PS00014; ER_TARGET; UNKNOWN_1.
KW Signal.
FT SIGNAL 1 19 POTENTIAL.
FT CHAIN 20 421 CALRETICULIN.
SQ SEQUENCE 421 AA; 48822 MW; 172C664F59F41F93 CRC64;

Query Match 89.4%; Score 169; DB 5; Length 421;
Best Local Similarity 88.6%; Pred. No. 1.7e-15;
Matches 31; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 VIPNYGKNVLINKDIRCKDDFTHLYTLIVRPDN 35
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DB 145 VIPNYGKNLLIKKDIRCKDDFTHLYTLIVKSDN 179

RESULT 3
Q26268
ID Q26268 PRELIMINARY; PRT; 405 AA.
AC Q26268;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE CALRTICULIN.
OS Aplysia californica (California sea hare).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Opisthobranchia; Anaspidae;
OC Aplysiidae; Aplysia.
OX NCBI_TaxID 6500;
RN [1]
RP SEQUENCE FROM N.A.
KA MEDLINE 93098937; PubMed 1463604;
KA Kennedy T.E., Kuhl D., Barzilai A., Sweatt J.D., Kandel E.R.;
RT "Long-term sensitization training in Aplysia leads to an increase in
RT calreticulin, a major presynaptic calcium-binding protein.";
RL Neuron 9:1013-1024(1992).
DR EMBL; S51239; AAB24569.1; -
DR InterPro; IPR000886; ER_target.
DR InterPro; IPR001580; Calreticulin.
DR Pfam; PF00262; calreticulin; 1.
DR PRINTS; PR00626; CALRETICULIN.
DR ProDom; PD001866; Calreticulin; 1.
DR PROSITE; PS00803; CALRETICULIN_1; 1.
DR PROSITE; PS00804; CALRETICULIN_2; 1.
DR PROSITE; PS00805; CALRETICULIN_REPEAT; 3.
DR PROSITE; PS00014; ER_TARGET; UNKNOWN_1.
SQ SEQUENCE 405 AA; 46738 MW; 14CAA201840D1D69 CRC64;
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Query Match 88.9%; Score 168; DB 5; Length 405;
Best Local Similarity 85.7%; Pred. No. 2.2e-15;
Matches 30; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 VIPNYGKNVLINKDIRCKDDFTHLYTLIVRPDN 35
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DB 142 VIPNYGKNLLVKKDIRCKDDVFSHLYTLIVRPDN 176

RESULT 4
Q16893
ID Q16893 PRELIMINARY; PRT; 410 AA.
AC Q16893;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-JAN-1999 (TrEMBLrel. 09, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE CALRETICULIN.
GN CRT-1.
OS Amblyomma americanum.
OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Acari;
OC Parasitiformes; Ixodida; Ixodidae; Amblyomma.
OX NCBI_TaxID-6943;
RN [1]
RP SEQUENCE OF 49-410 FROM N.A.
RC TISSUE: SALIVARY GLANDS;
RA Jaworski D.C.; Simmen F.A.; Lamoreaux W.J.; Coons L.B.; Muller M.T.;
RA Needham G.R.;
RT "A secreted calreticulin protein in Ixodid tick (Amblyomma americanum)
RT saliva";
RT J. Insect Physiol. 41:369-375(1995).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE: SALIVARY GLANDS;
RA Jaworski D.C.;
RL Submitted (MAR-1994) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE: SALIVARY GLANDS;
RA Pain-Thornton J.M.; Jaworski D.C.; Needham G.R.;
RL Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
EMBL; U07708; AAC79094.1; -
DR InterPro; IPR000886; ER_target.
DR InterPro; IPR001580; Calreticulin.
DR Pfam; PF00262; calreticulin; 1.
DR PRINTS; PR00626; CALRETICULIN.
DR ProDom; PD001866; Calreticulin; 1.
DR PROSITE; PS00803; CALRETICULIN_1; 1.
DR PROSITE; PS00805; CALRETICULIN_REPEAT; 3.
DR PROSITE; PS00014; ER_TARGET; UNKNOWN_1.
SQ SEQUENCE 410 AA; 47485 MW; 32CCB8750A17DC54 CRC64;

Query Match 88.9%; Score 168; DB 5; Length 410;
Best Local Similarity 88.6%; Pred. No. 2.2e-15;
Matches 31; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 VIPNYGKNVLINKDIRCKDDFTHLYTLIVRPDN 35
|||||:|:| | | | | | | | | | | | | | | | | |
DB 145 VIPNYGKNHLINKDIRCKDDVFTHLYTLIVKPDN 179

RESULT 5
Q91711
ID Q91711 PRELIMINARY; PRT; 343 AA.
AC Q91711;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE CALRETICULIN (FRAGMENT).
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
```

Query Match	85.2%;	Score 161;	DB 13;	Length 411;
Best Local Similarity	85.7%;	Pred. No. 2.1e-14;		

DR EMBL; AF195882; AAF13700.1; -;
DR InterPro; IPR000886; ER_target.
DR InterPro; IPR001580; Calreticulin.
DR Pfam; PF00262; calreticulin; 1.

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DR PRINTS; PR00626; CALRETICULIN.
DR PRODM; PD001866; Calreticulin; 1.
DR PROSITE; PS00803; CALRETICULIN_1; 1.
DR PROSITE; PS00804; CALRETICULIN_2; 1.
DR PROSITE; PS00805; CALRETICULIN_REPEAT; 3.
DR PROSITE; PS00014; ER_TARGET; UNKNOWN_1.
SQ SEQUENCE 417 AA; 48723 MW; 2000C5B4004699B6 CRC64;

Query Match
Best Local Similarity 81.5%; Score 154; DB 13; Length 417;
Matches 28; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 VIFNYGKGNVLINKDIRCKDDETHLYTLIVRPD 34
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Db 146 VIFNYGQNHLLIKDKCKDDELTHLYTLILRPD 179

RESULT 9
Q26514
ID Q26514 PRELIMINARY; PRT; 350 AA.
AC Q26514;
DT 01-NOV-1996 (TRENBLrel. 01, Created)
DT 01-NOV-1996 (TRENBLrel. 01, Last sequence update)
DT 01-JUN-2001 (TRENBLrel. 17, Last annotation update)
DE CALRETICULIN (FRAGMENT).
GN RAL-1.
OS Schistosoma japonicum (Blood fluke).
OC Eukaryota; Metazoa; Platyhelminthes; Neodermata;
OC Trematoda; Digenea; Strigeidida; Schistosomatoidea; Schistosomatidae;
OC Schistosoma.
OX NCBI_TaxID 6182;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN CHINESE;
RA Huggins M.C., Moloney N.A.;
RL Submitted (AUG-1993) to the EMBL/GenBank/DBJ databases.
DR EMBL; M80534; AAA29917.1; -.
DR InterPro; IPR000886; ER_target.
DR InterPro; IPR001580; Calreticulin.
DR Pfam; PF00262; Calreticulin; 1.
DR PRINTS; PR00626; CALRETICULIN.
DR PRODM; PD001866; Calreticulin; 1.
DR PROSITE; PS00803; CALRETICULIN_1; 1.
DR PROSITE; PS00804; CALRETICULIN_2; 1.
DR PROSITE; PS00805; CALRETICULIN_REPEAT; 1.
DR PROSITE; PS00014; ER_TARGET; UNKNOWN_1.
FT NON_TER 1
SQ SEQUENCE 350 AA; 40385 MW; 30FAB4E8BB685D1C CRC64;

Query Match
Best Local Similarity 81.0%; Score 153; DB 5; Length 350;
Matches 29; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 VIFNYGKGNVLINKDIRCKDDETHLYTLIVRPD 35
    |||||: || ||| ||||| |||||: |||
Db 99 VIFNYGQNHLLIKDKPKDQKTHLYTLIVRPD 133

RESULT 10
O45034
ID O45034 PRELIMINARY; PRT; 396 AA.
AC O45034;
DT 01-JUN-1998 (TRENBLrel. 06, Created)
DT 01-JUN-1998 (TRENBLrel. 06, Last sequence update)
DT 01-JUN-2001 (TRENBLrel. 17, Last annotation update)
DE CALRETICULIN.
OS Schistosoma japonicum (Blood fluke).
OC Eukaryota; Metazoa; Platyhelminthes; Neodermata;
OC Trematoda; Digenea; Strigeidida; Schistosomatoidea; Schistosomatidae;
OC Schistosoma.
OX NCBI_TaxID 6182;

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RN SEQUENCE FROM N.A.
RP STRAIN-PHILIPPINE (MINDORO);
RA Scott J.C.;
RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF044408; AAC0515.1; -.
DR InterPro; IPR000886; ER_target.
DR InterPro; IPR001580; Calreticulin.
DR Pfam; PF00262; calreticulin; 1.
DR PRINTS; PR00626; CALRETICULIN.
DR PRODM; PD001866; Calreticulin; 1.
DR PROSITE; PS00803; CALRETICULIN_1; 1.
DR PROSITE; PS00804; CALRETICULIN_2; 1.
DR PROSITE; PS00805; CALRETICULIN_REPEAT; 2.
DR PROSITE; PS00014; ER_TARGET; UNKNOWN_1.
SQ SEQUENCE 396 AA; 45813 MW; C57394C6FB4CD77B CRC64;

Query Match
Best Local Similarity 81.0%; Score 153; DB 5; Length 396;
Matches 29; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 VIFNYGKGNVLINKDIRCKDDETHLYTLIVRPD 35
    |||||: || ||| ||||| |||||: |||
Db 145 VIFNYGQNHLLIKDKPKDQKTHLYTLIVRPD 179

RESULT 11
O76961
ID O76961 PRELIMINARY; PRT; 403 AA.
AC O76961;
DT 01-NOV-1998 (TRENBLrel. 08, Created)
DT 01-NOV-1998 (TRENBLrel. 08, Last sequence update)
DT 01-JUN-2001 (TRENBLrel. 17, Last annotation update)
DE CALRETICULIN PRECURSOR.
GN CRT.
OS Necator americanus.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditiida; Strongylida;
OC Ancylostomatoidae; Ancylostomatidae; Bunostominae; Necator.
OX NCBI_TaxID-51031;
RN [1]
RP SEQUENCE FROM N.A.
RA Pritchard D.I., Brown A., McElroy P., Loukas A., Girdwood K.,
RA Berry C., Fullkrug R., Beck E.;
RT "Calreticulin is a hookworm allergen.";
RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ006790; CAA07254.1; -.
DR InterPro; IPR000886; ER_target.
DR InterPro; IPR001580; Calreticulin.
DR Pfam; PF00262; calreticulin; 1.
DR PRINTS; PR00626; CALRETICULIN.
DR PRODM; PD001866; Calreticulin; 1.
DR PROSITE; PS00803; CALRETICULIN_1; 1.
DR PROSITE; PS00804; CALRETICULIN_2; 1.
DR PROSITE; PS00805; CALRETICULIN_REPEAT; 3.
DR PROSITE; PS00014; ER_TARGET; UNKNOWN_1.
KW Signal; Allergen.
FT SIGNAL 1 16 POTENTIAL.
SQ SEQUENCE 403 AA; 46833 MW; 21F38B0515487B6F CRC64;

Query Match
Best Local Similarity 81.0%; Score 153; DB 5; Length 403;
Matches 28; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 2 IFNYGKGNVLINKDIRCKDDETHLYTLIVRPD 35
    ||: ||||| || ||||| |||||: |||
Db 143 IFSYGKGNHLLIKDKCKDDELTHLYTLILNPD 176

RESULT 12
Q98984
ID Q98984 PRELIMINARY; PRT; 419 AA.

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AC Q98984;
 DT 01-FEB-1997 (TREMBLrel. 02, Created)
 DT 01-FEB-1997 (TREMBLrel. 02, Last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
 DE CALRETICULIN.
 OS Rana rugosa (Frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Rana.
 OX NCBI_TaxID=84110;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96234004; PubMed=8654561;
 RA Yamamoto S., Nakamura M.: Cloning and expression in the liver of the
 RT "Calnexin: its molecular cloning and expression in the liver of the
 RT frog, Rana rugosa.";
 RL FEBS Lett. 387:27-32(1996).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Yamamoto S.;
 RT "Strong expression of the calreticulin gene in the liver of Rana
 RT rugosa tadpoles.";
 RL J. Exp. Zool. 0:0-0(1996).
 DR EMBL; D78589; BAAL1425.1; -;
 DR InterPro; IPR000896; ER_target.
 DR InterPro; IPR001580; Calreticulin.
 DR Pfam; PF00262; calreticulin; 1.
 DR PRINTS; PR00626; CALRETICULIN.
 DR ProDom; PD001866; Calreticulin; 1.
 DR PROSITE; PS00803; CALRETICULIN_1; 1.
 DR PROSITE; PS00804; CALRETICULIN_2; 1.
 DR PROSITE; PS00805; CALRETICULIN_REPEAT; 3.
 DR PROSITE; PS00014; ER_TARGET; UNKNOWN_1.
 SQ SEQUENCE 419 AA; 48658 MW; 2C857036769673BF CRC64;

 Query Match 78.3%; Score 148; DB 13; Length 419;
 Best Local Similarity 80.0%; Pred. No. 1.4e-12;
 Matches 28; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

 QY 1 VIFNYGKGNVLNKDIRCKDDETHLYTLIVRPDN 35
 DB 147 VIFNYGKGNLQINKDIRSKADYISHLYTLIVRPDN 181

 RESULT 13
 O18478 PRELIMINARY; PRT; 375 AA.
 AC O18478;
 DT 01-JAN-1998 (TREMBLrel. 05, Created)
 DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
 DE RAL-1 PROTEIN (FRAGMENT).
 OS Litomosoides sigmodontis.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea;
 OC Onchocercidae; Litomosoides.
 OX NCBI_TaxID=42156;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MacLennan K., Hoffman W.H., Taylor D.W.;
 RL Submitted (SEP-1997) to the EMBL/Genbank/DBJ databases.
 DR EMBL; AJ001621; CAA04877.1; -;
 DR InterPro; IPR001580; Calreticulin.
 DR Pfam; PF00262; calreticulin; 1.
 DR PRINTS; PR00626; CALRETICULIN.
 DR ProDom; PD001866; Calreticulin; 1.
 DR PROSITE; PS00803; CALRETICULIN_1; 1.
 DR PROSITE; PS00804; CALRETICULIN_2; 1.
 DR PROSITE; PS00805; CALRETICULIN_REPEAT; 3.
 FT NON_TER 375 375
 SQ SEQUENCE 375 AA; 43842 MW; 03F7642FBFF7A5B8 CRC64;

 Query Match 77.2%; Score 146; DB 5; Length 375;

Best Local Similarity 77.1%; Pred. No. 2.4e-12;
 Matches 27; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

 QY 1 VIFNYGKGNVLNKDIRCKDDETHLYTLIVRPDN 35
 DB 144 VIFHYKGRNHMKKDIRCKDDVETHLYTLIVNSDN 178

 RESULT 14
 O97372 PRELIMINARY; PRT; 387 AA.
 AC O97372;
 DT 01-MAY-1999 (TREMBLrel. 10, Created)
 DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
 DE CALRETICULIN PRECURSOR.
 OS Dirofilaria immitis.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea;
 OC Onchocercidae; Dirofilaria.
 OX NCBI_TaxID=6287;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99094497; PubMed=9879888;
 RA Tsuji N., Morales T.H., Ozols V.V., Carmody A.B., Chandrashekar R.;
 RT "Molecular characterization of a calcium-binding protein from the
 RT filarial parasite Dirofilaria immitis.";
 RL Mol. Biochem. Parasitol. 97:69-79(1998).
 DR EMBL; AF052978; AAD03405.1; -;
 DR InterPro; IPR001580; Calreticulin.
 DR Pfam; PF00262; calreticulin; 1.
 DR PRINTS; PR00626; CALRETICULIN.
 DR ProDom; PD001866; Calreticulin; 1.
 DR PROSITE; PS00803; CALRETICULIN_1; 1.
 DR PROSITE; PS00804; CALRETICULIN_2; 1.
 DR PROSITE; PS00805; CALRETICULIN_REPEAT; 3.
 KW Signal.
 FT SIGNAL 1 18 POTENTIAL.
 FT CHAIN 19 387 CALRETICULIN.
 SQ SEQUENCE 387 AA; 44941 MW; E7741BF6AAFA5885 CRC64;

 Query Match 77.2%; Score 146; DB 5; Length 387;
 Best Local Similarity 77.1%; Pred. No. 2.4e-12;
 Matches 27; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

 QY 1 VIFNYGKGNVLNKDIRCKDDETHLYTLIVRPDN 35
 DB 144 VIFHYKGRNHMKKDIRCKDDVETHLYTLIVNSDN 178

 RESULT 15
 Q9U5G0 PRELIMINARY; PRT; 321 AA.
 AC Q9U5G0;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
 DE CALRETICULIN (FRAGMENT).
 OS Eptatretus burgeri (Inshore hagfish).
 OC Eukaryota; Metazoa; Chordata; Craniata; Hyperotreti; Myxiniiformes;
 OC Myxiniidae; Eptatretinae; Eptatretus.
 OX NCBI_TaxID=7764;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=LIVER;
 RX MEDLINE=20063780; PubMed=10594174;
 RA Kuraku S., Hoshiyama D., Katoh K., Suga H., Miyata T.;
 RT "Monophyly of lampreys and hagfishes supported by nuclear DNA-coded
 RT genes.";
 RL J. Mol. Evol. 49:729-735(1999).
 DR EMBL; AB025323; BAA88476.1; -;
 DR InterPro; IPR000886; ER_target.
 DR InterPro; IPR001580; Calreticulin.

DR Pfam; PF00262; calreticulin; 1.
DR PRINTS; PR00626; CALRETICULIN.
DR ProDom; PD001866; Calreticulin; 1.
DR PROSITE; PS00804; CALRETICULIN_2; 1.
DR PROSITE; PS00805; CALRETICULIN_REPEAT; 3.
DR PROSITE; PS00014; ER_TARGET; UNKNOWN_1.
FT NON_TER 1
SQ SEQUENCE 321 AA; 37367 MW; 6E8DFA98D42F7AEF CRC64;

Query Match 67.7%; Score 128; DB 13; Length 321;
Best Local similarity 67.6%; Pred. No. 6.4e-10;
Matches 23; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

QY 1 VIFNYKKNVLLINKDIRCKDDETHLYTLIVRPD 34
DB 45 VILNSKGNHLIKKVKCKDDETHLYTLMLYPD 78

Search completed: January 9, 2002, 15:03:30
Job time: 272 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: January 9, 2002, 15:01:13 ; Search time 83.2 Seconds
(without alignments)
31.161 Million cell updates/sec

Title: US-09-828-000-7
Perfect score: 189
Sequence: 1 VIFNYGKNVLINKDIRCKDDETHLYTLIVRPDN 35

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 522463 seqs, 74073290 residues

Total number of hits satisfying chosen parameters: 522463

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_1101.*
1: /SID88/gcgdata/geneseq/geneseqp/AA1980.DAT.*
2: /SID88/gcgdata/geneseq/geneseqp/AA1981.DAT.*
3: /SID88/gcgdata/geneseq/geneseqp/AA1982.DAT.*
4: /SID88/gcgdata/geneseq/geneseqp/AA1983.DAT.*
5: /SID88/gcgdata/geneseq/geneseqp/AA1984.DAT.*
6: /SID88/gcgdata/geneseq/geneseqp/AA1985.DAT.*
7: /SID88/gcgdata/geneseq/geneseqp/AA1986.DAT.*
8: /SID88/gcgdata/geneseq/geneseqp/AA1987.DAT.*
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20: /SID88/gcgdata/geneseq/geneseqp/AA1999.DAT.*
21: /SID88/gcgdata/geneseq/geneseqp/AA2000.DAT.*
22: /SID88/gcgdata/geneseq/geneseqp/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	189	100.0	60	21	Recombinant human
2	189	100.0	61	21	Recombinant human
3	189	100.0	180	21	Human vasostatin (
4	189	100.0	280	21	Recombinant delta-
5	189	100.0	400	21	Recombinant human
6	189	100.0	401	18	Calreticulin, Hom
7	189	100.0	417	10	60 kD Ro (Ro/SSA)
8	189	100.0	417	20	Calreticulin, Hom
9	189	100.0	417	21	Human MBP-calretic
10	175	92.6	49	21	Recombinant human
11	167	88.4	403	17	Flea calreticulin

12	139	73.5	336	12	AAR12312	Partial sequence o
13	107	56.6	122	20	AAV00924	Human cClqR bindin
14	107	56.6	122	20	AAV00926	Rat cClqR binding
15	105	55.6	415	22	AAB66341	Castor bean calret
16	105	55.6	415	22	AAB66343	Castor bean calret
17	99	52.4	122	20	AAV00925	Mouse cClqR bindin
18	98	51.9	385	21	AAB32385	Human secreted pro
19	97	51.3	312	21	AAG24609	Arabidopsis thalia
20	97	51.3	312	21	AAG47933	Arabidopsis thalia
21	97	51.3	332	21	AAG30998	Arabidopsis thalia
22	97	51.3	421	21	AAG24608	Arabidopsis thalia
23	97	51.3	421	21	AAG47932	Arabidopsis thalia
24	97	51.3	424	21	AAG24607	Arabidopsis thalia
25	97	51.3	424	21	AAG47931	Arabidopsis thalia
26	97	51.3	441	21	AAG30997	Arabidopsis thalia
27	97	51.3	444	21	AAG30996	Arabidopsis thalia
28	63	33.3	593	16	AAR71094	Calnexin sequence.
29	58	31.0	417	21	AAV77953	A. thaliana enviro
30	58	30.7	542	22	AAB66342	Castor bean calnex
31	54	28.6	394	21	AAG26285	Arabidopsis thalia
32	54	28.6	394	21	AAG45612	Arabidopsis thalia
33	54	28.6	530	21	AAG26284	Arabidopsis thalia
34	54	28.6	530	21	AAG45611	Arabidopsis thalia
35	54	28.6	567	21	AAG45610	Arabidopsis thalia
36	51	27.0	458	21	AAB40855	Human ORFX ORF619
37	51	27.0	848	21	AAV88565	Human NCAM 140kD i
38	50.5	26.7	236	18	AAW26427	Swinepox virus Hin
39	50.5	26.7	236	22	AAB68248	Protein encoded by
40	50	26.5	1188	21	AAB18183	Plasmodium falcipa
41	49	25.9	318	20	AAV28509	Fen(Y205D) mutant
42	49	25.9	346	22	AAG93016	C glycosylated prote
43	48	25.4	17	20	AAV21879	Peptide Seq ID No:
44	48	25.4	17	20	AAV09101	Cell adhesion reco
45	48	25.4	17	21	AAV78215	N-CAM heparin bind

ALIGNMENTS

RESULT 1
ID AAY92354 standard; Protein; 60 AA.
XX
AC AAY92354;
XX
DT 10-AUG-2000 (first entry)
XX
DE Recombinant human calreticulin residues 121-180.

XX MBP-calreticulin; maltose binding protein; angiogenesis; inhibition;
XX endothelial cell; anti-angiogenic; neuroprotective; antidiabetic;
KW cytostatic; dermalogical; immunosuppressive; antiinflammatory; hepatic;
KW anti-atherosclerotic; gastrointestinal; anti-arthritis; ophthalmic.

XX Homo sapiens.
OS Synthetic.

XX WO2000020577-A1.

XX 13-APR-2000.

XX 05-OCT-1999; 99WO-US23240.

XX 06-OCT-1998; 98US-0103438.

XX (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX Tosato G, Pike SE, Yao L;

XX WPI; 2000-303767/26.

XX Inhibiting endothelial cell growth and angiogenesis using calreticulin,
PT useful for suppressing tumor growth

XX PS Claim 4; Page 85; 99pp; English.

XX CC A novel method of inhibiting endothelial cell growth comprises

XX CC contacting the cells with calreticulin (or its fragments/variants).

XX CC Fragments of calreticulin causes at least 40% inhibition of angiogenesis,

XX CC tumor growth and/or endothelial cell growth (claimed). The method may be

XX CC used for inhibiting angiogenesis in a patient. The angiogenesis is

XX CC associated with a disease other than a tumor that is associated with

XX CC neovascularization (e.g. diabetic neuropathy, retrolental fibroplasia,

XX CC trachoma, neovascular glaucoma, psoriasis, angiofibromas, immune

XX CC inflammation, atherosclerosis, excessive wound repair, retinal

XX CC neovascularization, macular degeneration, corneal graft rejection,

XX CC contact lens overwear, Crohn's disease, non-immune inflammation,

XX CC rheumatoid arthritis, systemic lupus erythematosus, thyroiditis,

XX CC Goodpasture's syndrome, systemic vasculitis, scleroderma, Sjorgen's

XX CC syndrome, sarcoidosis and primary biliary cirrhosis). The method may

XX CC also be used for treating/inhibiting tumor growth especially

XX CC Kaposi's sarcoma (claimed).

SQ Sequence 60 AA;

Query Match 100.0%; Score 189; DB 21; Length 60;

Best Local Similarity 100.0%; Pred. No. 1.3e-22;

Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VIFNYGKNVLINKDIRCKDDETHLYTLIVRPDN 35

DB 9 VIFNYGKNVLINKDIRCKDDETHLYTLIVRPDN 43

RESULT 2

AAI92352

ID AAY92352 standard; Protein; 61 AA.

XX AC AAY92352;

XX 10-AUG-2000 (first entry)

XX Recombinant human calreticulin residues 120-180.

XX MBP-calreticulin; maltose binding protein; angiogenesis; inhibition;

KW endothelial cell; anti-angiogenic; neuroprotective; antidiabetic;

KW cytotatic; dermalogical; immunosuppressive; antiinflammatory; hepatic;

KW anti-atherosclerotic; gastrointestinal; anti-arthritis; ophthalmic.

XX OS Homo sapiens.

OS Synthetic.

XX WO200020577-A1.

XX 13-APR-2000.

XX 05-OCT-1999; 99WO-US23240.

XX 06-OCT-1998; 98US-0103438.

XX (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX Tosato G, Pike SE, Yao L;

XX WPI; 2000-303767/26.

XX Inhibiting endothelial cell growth and angiogenesis using calreticulin,

PT useful for suppressing tumor growth

XX Claim 4; Page 82-83; 99pp; English.

XX A novel method of inhibiting endothelial cell growth comprises

XX contacting the cells with calreticulin (or its fragments/variants).

XX Fragments of calreticulin causes at least 40% inhibition of angiogenesis,

XX tumor growth and/or endothelial cell growth (claimed). The method may be

XX associated with a disease other than a tumor that is associated with

XX neovascularization (e.g. diabetic neuropathy, retrolental fibroplasia,

XX trachoma, neovascular glaucoma, psoriasis, angiofibromas, immune

XX inflammation, atherosclerosis, excessive wound repair, retinal

XX tumor growth and/or endothelial cell growth (claimed). The method may be

CC used for inhibiting angiogenesis in a patient. The angiogenesis is

CC associated with a disease other than a tumor that is associated with

CC neovascularization (e.g. diabetic neuropathy, retrolental fibroplasia,

CC trachoma, neovascular glaucoma, psoriasis, angiofibromas, immune

CC inflammation, atherosclerosis, excessive wound repair, retinal

CC neovascularization, macular degeneration, corneal graft rejection,

CC contact lens overwear, Crohn's disease, non-immune inflammation,

CC rheumatoid arthritis, systemic lupus erythematosus, thyroiditis,

CC Goodpasture's syndrome, systemic vasculitis, scleroderma, Sjorgen's

CC syndrome, sarcoidosis and primary biliary cirrhosis). The method may

CC also be used for treating/inhibiting tumor growth especially

XX Kaposi's sarcoma (claimed).

SQ Sequence 61 AA;

Query Match 100.0%; Score 189; DB 21; Length 61;

Best Local Similarity 100.0%; Pred. No. 1.3e-22;

Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VIFNYGKNVLINKDIRCKDDETHLYTLIVRPDN 35

DB 10 VIFNYGKNVLINKDIRCKDDETHLYTLIVRPDN 44

RESULT 3

AAI92351

ID AAY92351 standard; Protein; 180 AA.

XX AC AAY92351;

XX 10-AUG-2000 (first entry)

XX Human vasostatin (calreticulin N-terminal 180 amino acids).

XX MBP-calreticulin; maltose binding protein; vasostatin; N-terminal;

KW angiogenesis; inhibition; endothelial cell; anti-angiogenic;

KW neuroprotective; antidiabetic; cytostatic; dermalogical; hepatic;

KW immunosuppressive; antiinflammatory; anti-atherosclerotic;

KW gastrointestinal; anti-arthritis; ophthalmic.

XX OS Homo sapiens.

OS Synthetic.

XX WO200020577-A1.

XX 13-APR-2000.

XX 05-OCT-1999; 99WO-US23240.

XX 06-OCT-1998; 98US-0103438.

XX (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX Tosato G, Pike SE, Yao L;

XX WPI; 2000-303767/26.

Inhibiting endothelial cell growth and angiogenesis using calreticulin,

PT useful for suppressing tumor growth

XX Claim 4; Page 82; 99pp; English.

XX A novel method of inhibiting endothelial cell growth comprises

XX contacting the cells with calreticulin (or its fragments/variants).

XX Fragments of calreticulin causes at least 40% inhibition of angiogenesis,

XX tumor growth and/or endothelial cell growth (claimed). The method may be

XX used for inhibiting angiogenesis in a patient. The angiogenesis is

XX associated with a disease other than a tumor that is associated with

XX neovascularization (e.g. diabetic neuropathy, retrolental fibroplasia,

XX trachoma, neovascular glaucoma, psoriasis, angiofibromas, immune

XX inflammation, atherosclerosis, excessive wound repair, retinal

XX tumor growth and/or endothelial cell growth (claimed). The method may be

CC contact lens overwear, Crohn's disease, non-immune inflammation,
 CC rheumatoid arthritis, systemic lupus erythematosus, thyroiditis,
 CC Goodpasture's syndrome, systemic vasculitis, scleroderma, Sjorgen's
 CC syndrome, sarcoidosis and primary biliary cirrhosis). The method may
 CC also be used for treating/inhibiting tumor growth especially
 CC Kaposi's sarcoma (claimed).
 XX
 SQ Sequence 180 AA;

Query Match 100.0%; Score 189; DB 21; Length 180;
 Best Local Similarity 100.0%; Pred. No. 4.9e-22;
 Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VIFNYGKNVLINKDIRCKDDEFTHTLTLIVRPDN 35
 Db 129 vfnygknvlinkdirckddefthlytlivrpdn 163
 |||

RESULT 4
 AAY92355
 ID AAY92355 standard; Protein; 280 AA.
 XX
 AC AAY92355;
 XX
 DT 10-AUG-2000 (first entry)
 XX
 DE Recombinant delta-120 calreticulin.
 XX
 KW MBP-calreticulin; maltose binding protein; angiogenesis; inhibition;
 KW endothelial cell; anti-angiogenic; neuroprotective; antidiabetic;
 KW cytostatic; dermalogical; immunosuppressive; antiinflammatory; hepatic;
 KW anti-atherosclerotic; gastrointestinal; anti-arthritis; ophthalmic.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 PN WO200020577-A1.
 XX
 PD 13-APR-2000.
 XX
 PF 05-OCT-1999; 99WO-US23240.
 XX
 PR 06-OCT-1998; 98US-0103438.
 XX
 PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
 XX
 PI Tosato G, Pike SE, Yao L;
 XX
 DR WPI; 2000-303767/26.
 XX
 PT Inhibiting endothelial cell growth and angiogenesis using calreticulin,
 PT useful for suppressing tumor growth
 XX
 PS Claim 4; Page 86; 99pp; English.
 XX
 CC This sequence comprises recombinant human calreticulin (AAY92350)
 CC missing the N-terminal 120 amino acids.
 CC A novel method of inhibiting endothelial cell growth comprises
 CC contacting the cells with calreticulin (or its fragments/variants).
 CC Fragments of calreticulin causes at least 40% inhibition of
 CC angiogenesis, tumor growth and/or endothelial cell growth (claimed). The
 CC method may be used for inhibiting angiogenesis in a patient. The
 CC angiogenesis is associated with a disease other than a tumor that is
 CC associated with neovascularization (e.g. diabetic neuropathy, retrolental
 CC fibroplasia, trachoma, neovascular glaucoma, psoriasis, angiofibromas,
 CC immune inflammation, atherosclerosis, excessive wound repair, retinal
 CC neovascularization, macular degeneration, corneal graft rejection,
 CC contact lens overwear, Crohn's disease, non-immune inflammation,
 CC rheumatoid arthritis, systemic lupus erythematosus, thyroiditis,
 CC Goodpasture's syndrome, systemic vasculitis, scleroderma, Sjorgen's
 CC syndrome, sarcoidosis and primary biliary cirrhosis). The method may
 CC also be used for treating/inhibiting tumor growth especially

CC Kaposi's sarcoma (claimed).
 XX
 SQ Sequence 280 AA;

Query Match 100.0%; Score 189; DB 21; Length 280;
 Best Local Similarity 100.0%; Pred. No. 8.4e-22;
 Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VIFNYGKNVLINKDIRCKDDEFTHTLTLIVRPDN 35
 Db 9 vfnygknvlinkdirckddefthlytlivrpdn 43
 |||

RESULT 5
 AAY92350
 ID AAY92350 standard; Protein; 400 AA.
 XX
 AC AAY92350;
 XX
 DT 10-AUG-2000 (first entry)
 XX
 DE Recombinant human MBP-calreticulin.
 XX
 KW MBP-calreticulin; maltose binding protein; angiogenesis; inhibition;
 KW endothelial cell; anti-angiogenic; neuroprotective; antidiabetic;
 KW cytostatic; dermalogical; immunosuppressive; antiinflammatory; hepatic;
 KW anti-atherosclerotic; gastrointestinal; anti-arthritis; ophthalmic.
 XX
 OS Homo sapiens.
 PN WO200020577-A1.
 XX
 PD 13-APR-2000.
 XX
 PF 05-OCT-1999; 99WO-US23240.
 XX
 PR 06-OCT-1998; 98US-0103438.
 XX
 PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
 XX
 PI Tosato G, Pike SE, Yao L;
 XX
 DR WPI; 2000-303767/26.
 XX
 PR N-PSDB; AAA09346, AAA09347.
 XX
 PT Inhibiting endothelial cell growth and angiogenesis using calreticulin,
 PT useful for suppressing tumor growth
 XX
 PS Claim 4; Page 80-81; 99pp; English.
 XX
 CC Recombinant human MBP-calreticulin comprises the sequence of human
 CC calreticulin (see AAY92349) without the 17 N-terminal amino acids.
 CC A novel method of inhibiting endothelial cell growth comprises
 CC contacting the cells with calreticulin (or its fragments/variants).
 CC Fragments of calreticulin causes at least 40% inhibition of
 CC angiogenesis, tumor growth and/or endothelial cell growth (claimed). The
 CC method may be used for inhibiting angiogenesis in a patient. The
 CC angiogenesis is associated with a disease other than a tumor that is
 CC associated with neovascularization (e.g. diabetic neuropathy, retrolental
 CC fibroplasia, trachoma, neovascular glaucoma, psoriasis, angiofibromas,
 CC immune inflammation, atherosclerosis, excessive wound repair, retinal
 CC neovascularization, macular degeneration, corneal graft rejection,
 CC contact lens overwear, Crohn's disease, non-immune inflammation,
 CC rheumatoid arthritis, systemic lupus erythematosus, thyroiditis,
 CC Goodpasture's syndrome, systemic vasculitis, scleroderma, Sjorgen's
 CC syndrome, sarcoidosis and primary biliary cirrhosis). The method may
 CC also be used for treating/inhibiting tumor growth especially
 CC Kaposi's sarcoma (claimed).
 XX
 SQ Sequence 400 AA;

Query Match 100.0%; Score 189; DB 21; Length 400;
 Best Local Similarity 100.0%; Pred. No. 1.3e-21;
 Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VIFNYGKNVINKDIRCKDDETHLYTLIVRPDN 35
 |||
 Db 129 vifnygknvlnkdrckddethlytlivrpdn 163

RESULT 6

AAW11156
 ID AAW11156 standard; peptide; 401 AA.

XX
 AC AAW11156;

DT 31-MAY-1997 (first entry)

XX Calreticulin.

XX calreticulin; C-domain; restenosis; inhibitor.

XX Homo sapiens.

XX WO9636643-A1.

XX 21-NOV-1996.

XX 17-MAY-1996; 96WO-IB00471.

XX 16-MAY-1996; 96US-0649417.

XX 17-MAY-1995; 95US-0442844.

XX (UYAL-) UNIV ALBERTA.

XX Lucas A, Michalak M;

XX WPI; 1997-012036/01.

XX Inhibition of restenosis in patients - using calreticulin or a
 PT C-domain polypeptide of calreticulin or a variant with the same
 PT activity.

XX Disclosure; Fig 1; 48pp; English.

XX The present sequence is calreticulin. It and a C-domain derived peptide
 CC (AAW06736) are useful for treating a patient to inhibit restenosis. The
 CC calreticulin-type cpds. are administered either parenterally,
 CC intravenously or via a catheter and can target areas of vascular damage
 CC to inhibit or prevent restenosis.

XX Sequence 401 AA;

Query Match 100.0%; Score 189; DB 18; Length 401;
 Best Local Similarity 100.0%; Pred. No. 1.3e-21;
 Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VIFNYGKNVINKDIRCKDDETHLYTLIVRPDN 35
 |||
 Db 129 vifnygknvlnkdrckddethlytlivrpdn 163

RESULT 7

AAW92276

ID AAW92276 standard; protein; 417 AA.

XX
 AC AAW92276;

DT 23-FEB-1990 (first entry)

XX 60 kD Ro (Ro/SSA) antigen.

XX Sjogren's syndrome; systemic lupus erythematosus.

XX Synthetic.
 OS WO8909273-A.
 PN 05-OCT-1989.
 PD 22-MAR-1989; 89WO-US01213.
 PE 22-MAR-1988; 88US-0171634.
 PR (TEXA) UNIV OF TEXAS SYST.
 XX Sontheimer RD, Capra JD, McCauliffe DP;
 PI WPI; 1989-309537/42.
 DR N-PSDB; AAP92276.
 XX DNA sequences encoding antigenic epitope(s) of Ro 60 kD autoantigen
 PT - used in immunoassays to detect rheumatic disease
 XX Disclosure; Fig 2; 88pp; English.
 XX Synthetic peptides corresp. to an epitopic core of Ro antigen are
 CC expressed recombinantly to detect autoantibodies, for identification
 CC of autoimmune diseases. These epitopes are AAS 24-36, 23-36, 188-209,
 CC or 241-255. The peptides may be substd. for ribonucleoprotein particle
 CC antigens.
 XX Sequence 417 AA;

Query Match 100.0%; Score 189; DB 10; Length 417;
 Best Local Similarity 100.0%; Pred. No. 1.4e-21;
 Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VIFNYGKNVINKDIRCKDDETHLYTLIVRPDN 35
 |||
 Db 146 vifnygknvlnkdrckddethlytlivrpdn 180

RESULT 8

AAW00927

ID AAW00927 standard; Protein; 417 AA.

XX
 AC AAW00927;

XX 28-MAY-1999 (first entry)

XX Calreticulin.

XX Clq and collectin receptor; cClqR binding domain; complement ublquitin;
 KW CUB functionality; inhibitor; complement activation; inflammation;
 KW myocardial infarction; brain ischaemia; gut ischaemia; amyloid plaque;
 KW rheumatoid arthritis; systemic lupus erythematosus; Alzheimer's disease;
 KW immune complex nephritis; therapy.

XX Homo sapiens.

XX WO9907406-A1.

XX 18-FEB-1999.

XX 12-AUG-1998; 98WO-GB02430.

XX 12-AUG-1997; 97GB-0016998.

XX (UYLE-) UNIV LEICESTER.

XX Schwaebler W;

XX WPI; 1999-180404/15.

CC added as the basis for a vaccine against blindness.

CC added as the basis for a vaccine against blindness.

SQ Sequence 336 AA;

Query Match 73.5%; Score 139; DB 12; Length 336;
 Best Local Similarity 74.3%; Pred. No. 9.2e-14;
 Matches 26; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 1 VIFNYKGNVLINKDIRCKDDFTHTLYTLIVRPDN 35
 ||||| : : ||||| ||||| ||
 Db 92 vifhykdnhmikdkrckddvfthtlytlivnsdn 126

RESULT 13

AYY00924
 ID AAY00924 standard; Protein; 122 AA.

XX AC AAY00924;

XX DT 28-MAY-1999 (first entry)

XX DE Human cClqR binding domain protein sequence.

XX KW Clq and collectin receptor; cClqR binding domain; complement ubiquitin;
 KW CUB functionality; inhibitor; complement activation; inflammation;
 KW myocardial infarction; brain ischaemia; gut ischaemia; amyloid plaque;
 KW rheumatoid arthritis; systemic lupus erythematosus; Alzheimer's disease;
 KW immune complex nephritis; therapy.

XX OS Homo sapiens.

XX PN W09907406-A1.

XX PD 18-FEB-1999.

XX PF 12-AUG-1998; 98WO-GB02430.

XX PR 12-AUG-1997; 97GB-0016998.

XX PA (UYLE-) UNIV LEICESTER.

XX PI Schwaeble W;

XX DR WPI; 1999-180404/15.

XX DR N-PSDB; AAX27251.

XX PT Use of a cClqR binding domain - to modulate complement ubiquitin
 PT (CUB) functionality.

XX PS Claim 9; Page 23; 31pp; English.

XX CC This sequence is a Clq and collectin receptor (cClqR) binding
 CC domain. The invention relates to the use of a cClqR binding domain in a
 CC medicament to effect complement ubiquitin (CUB) functionality, and an
 CC inhibitor of the cClqR binding domain in a medicament to inhibit CUB
 CC functionality. The cClqR binding domain, or its inhibitor, can be used to
 CC treat a human or animal body. Particularly an inhibitor is used to treat
 CC complement activation involved in the initiation and maintenance of
 CC inflammation, for example in myocardial infarction, brain ischaemia
 CC (stroke), gut ischaemia, rheumatoid arthritis, systemic lupus
 CC erythematosus, burns, immune complex nephritis, and to treat amyloid
 CC plaques in Alzheimer's disease. The use of cClqR binding domain or
 CC inhibitor enables the CUB domain functionality to be modulated using a
 CC low molecular weight molecule.

XX SQ Sequence 122 AA;

Query Match 56.6%; Score 107; DB 20; Length 122;
 Best Local Similarity 100.0%; Pred. No. 3.2e-09;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 17 RCKDDEFTHLYTLIVRPDN 35
 ||||| ||||| ||||| |||||

Db 1 rckddefthlytlivrpdn 19

RESULT 14

AYY00926
 ID AAY00926 standard; Protein; 122 AA.

XX AC AAY00926;

XX DT 28-MAY-1999 (first entry)

XX DE Rat cClqR binding domain protein sequence.

XX KW Clq and collectin receptor; cClqR binding domain; complement ubiquitin;
 KW CUB functionality; inhibitor; complement activation; inflammation;
 KW myocardial infarction; brain ischaemia; gut ischaemia; amyloid plaque;
 KW rheumatoid arthritis; systemic lupus erythematosus; Alzheimer's disease;
 KW immune complex nephritis; therapy.

XX OS Rattus norvegicus.

XX PN W09907406-A1.

XX PD 18-FEB-1999.

XX PF 12-AUG-1998; 98WO-GB02430.

XX PR 12-AUG-1997; 97GB-0016998.

XX PA (UYLE-) UNIV LEICESTER.

XX PI Schwaeble W;

XX DR WPI; 1999-180404/15.

XX DR N-PSDB; AAX27253.

XX PT Use of a cClqR binding domain - to modulate complement ubiquitin
 PT (CUB) functionality.

XX PS Claim 9; Page 24-25; 31pp; English.

XX CC This sequence is a Clq and collectin receptor (cClqR) binding
 CC domain. The invention relates to the use of a cClqR binding domain in a
 CC medicament to effect complement ubiquitin (CUB) functionality, and an
 CC inhibitor of the cClqR binding domain in a medicament to inhibit CUB
 CC functionality. The cClqR binding domain, or its inhibitor, can be used to
 CC treat a human or animal body. Particularly an inhibitor is used to treat
 CC complement activation involved in the initiation and maintenance of
 CC inflammation, for example in myocardial infarction, brain ischaemia
 CC (stroke), gut ischaemia, rheumatoid arthritis, systemic lupus
 CC erythematosus, burns, immune complex nephritis, and to treat amyloid
 CC plaques in Alzheimer's disease. The use of cClqR binding domain or
 CC inhibitor enables the CUB domain functionality to be modulated using a
 CC low molecular weight molecule.

XX SQ Sequence 122 AA;

Query Match 56.6%; Score 107; DB 20; Length 122;
 Best Local Similarity 100.0%; Pred. No. 3.2e-09;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 17 RCKDDEFTHLYTLIVRPDN 35
 ||||| ||||| ||||| |||||

Db 1 rckddefthlytlivrpdn 19

RESULT 15

AAB66341
 ID AAB66341 standard; Protein; 415 AA.

XX AC AAB66341;

XX

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: January 9, 2002, 15:03:28 ; Search time 78.15 Seconds
(without alignments)
33.690 Million cell updates/sec

Title: US-09-828-000-6
Perfect score: 96
Sequence: 1 VIFNYKGNVLINKDIRC 18

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 473505 seqs, 146272329 residues

Total number of hits satisfying chosen parameters: 473505

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_17:*
1: sp-archaea:*
2: sp-bacteria:*
3: sp-fungi:*
4: sp-human:*
5: sp-invertebrate:*
6: sp-mammal:*
7: sp-mhc:*
8: sp-organelle:*
9: sp-phage:*
10: sp-plant:*
11: sp-rodent:*
12: sp-virus:*
13: sp-invertebrate:*
14: sp-unclassified:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	89	92.7	318	13 Q9PTX7	Q9ptx7 lampetra re
2	87	90.6	421	5 Q9U6S0	Q9u6s0 strongyloce
3	86	89.6	405	5 Q26268	Q26268 aplysia cal
4	85	88.5	410	5 Q16893	Q16893 amblyomma a
5	79	82.3	406	5 Q9U916	Q9u916 drosophila
6	78	81.2	419	13 Q98984	Q98984 rana rugosa
7	76	79.2	417	13 Q9PUC1	Q9pucl brachydanio
8	74	77.1	403	5 Q76961	Q76961 necator ame
9	73	76.0	343	13 Q91711	Q91711 xenopus lae
10	73	76.0	375	5 Q18478	Q18478 litomosoid
11	73	76.0	387	5 Q97372	Q97372 dirofilaria
12	73	76.0	411	13 Q91710	Q91710 xenopus lae
13	72	75.0	350	5 Q26514	Q26514 schistosoma
14	72	75.0	396	5 Q45034	Q45034 schistosoma
15	60	62.5	321	13 Q9U5G0	Q9u5g0 eptatretus
16	51	53.1	348	4 Q00557	Q00557 homo sapien
17	49	51.0	506	13 Q73736	Q73736 brachydanio
18	49	51.0	506	13 Q9DGI6	Q9dgi6 brachydanio
19	48	50.0	247	2 Q48830	Q48830 lactobacill

20	48	50.0	846	13	057577	057577 cynops pyrr
21	48	50.0	1100	13	057576	057576 cynops pyrr
22	47	49.0	725	13	073633	073633 xenopus lae
23	47	49.0	725	13	073634	073634 xenopus lae
24	46	47.9	576	10	Q9LUY5	Q9luY5 arabidopsis
25	45	46.9	412	10	Q40040	Q40040 hordeum vul
26	45	46.9	415	10	Q40041	Q40041 hordeum vul
27	45	46.9	501	1	057693	057693 thermoprote
28	44.5	46.4	339	10	Q9AW69	Q9aw69 guillardia
29	44.5	46.4	781	12	Q82857	Q82857 jembrana di
30	44	45.8	321	10	Q41799	Q41799 zea mays (m
31	44	45.8	421	10	Q43712	Q43712 zea mays (m
32	44	45.8	631	12	Q9DHM5	Q9dhm5 yaba-like d
33	43	44.8	103	1	058084	058084 pyrococcus
34	43	44.8	250	6	P79232	P79232 papio hamad
35	43	44.8	257	1	Q9UZY6	Q9uzy6 pyrococcus
36	43	44.8	270	2	Q44795	Q44795 borrelia bu
37	43	44.8	270	2	Q9L9N5	Q9l9n5 borrelia bu
38	43	44.8	318	10	Q40126	Q40126 lycopersico
39	43	44.8	372	8	Q9XPX5	Q9xpx5 spyrldium p
40	43	44.8	372	8	Q9XPX3	Q9xpx3 adolphia ca
41	43	44.8	395	8	Q9TNG4	Q9tnG4 datisca can
42	43	44.8	502	12	Q9ICT8	Q9ict8 chimpanzee
43	43	44.8	528	5	Q9UAF9	Q9uaf9 ephyddatia f
44	43	44.8	654	10	Q9SGI7	Q9sgI7 arabidopsis
45	43	44.8	743	10	Q9MAS2	Q9mas2 arabidopsis

ALIGNMENTS

RESULT 1
Q9PTX7
ID Q9PTX7 PRELIMINARY; PRT; 318 AA.
AC Q9PTX7;
DT 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TRENBLrel. 17, Last annotation update)
DE CALRETICULIN (FRAGMENT).
OS Lampetra reissneri.

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Hyperoartia;
OC Petromyzontiformes; Petromyzontidae; Lampetra.
OX NCBI_TaxID=7753;
RN [1]

RP SEQUENCE FROM N.A.
RX MEDLINE=20063780; PubMed=10594174;
RA Kuraku S., Hoshiyama D., Katoh K., Suga H., Miyata T.;

RT "Monophyly of lampreys and hagfishes supported by nuclear DNA-coded genes.";
RL J. Mol. Evol. 49:729-735(1999).
DR EMBL; AB025328; BAA88481.1; -;
DR InterPro; IPR000886; ER target.
DR InterPro; IPR001580; Calreticulin.
DR Pfam; PF00262; calreticulin; 1.
DR PRINTS; PRO0626; CALRETICULIN.
DR PRODOM; PD001866; Calreticulin; 1.
DR PROSITE; PS00804; CALRETICULIN.2; 1.
DR PROSITE; PS00805; CALRETICULIN-REPEAT; 3.
DR PROSITE; PS00014; ER-TARGET; UNKNOWN_1.

FT NON_TER 1
SQ SEQUENCE 318 AA; 36997 MW; C88102EA1CAC1506 CRC64;

Query Match 92.7%; Score 89; DB 13; Length 318;

Best Local Similarity 94.4%; Pred. No. 5.8e-06; Mismatches 1; Indels 0; Gaps 0;

Matches 17; Conservative 0;

Qy 1 VIFNYKGNVLINKDIRC 18

Db 45 VIFNYKGNVLINKDIRC 62

RESULT 2

Q9U6S0
ID Q9U6S0 PRELIMINARY; PRT; 421 AA.
AC Q9U6S0;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TReMBLrel. 17, Last annotation update)
DE CALRETICULIN PRECURSOR.
GN CALRPT.
OS Strongylocentrotus purpuratus (Purple sea urchin).
OC Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa; Strongylocentrotidae;
OC Echinozoa; Euechinozoa; Echinodermata; Echinozoa; Echinozoa; Strongylocentrotidae;
OC Strongylocentrotus.
OX NCBI_TaxID:7668;
RN [1]
RP SKOUNHCE FROM N.A.
RA Sunun J.M., Just M.L., Lennarz W.J.;
RT Cloning and Characterization of AlphaP Integrin and Calreticulin in
RT Embryos of the Sea Urchin.
RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF177915; AAD55725.1; -;
DR InterPro; IPR000886; ER_target.
DR Pfam; PF00262; Calreticulin; 1.
DR PRINTS; PR00626; CALRETICULIN.
DR ProDom; PD001866; Calreticulin; 1.
DR PROSITE; PS00804; CALRETICULIN_2; 1.
DR PROSITE; PS00805; CALRETICULIN_REPEAT; 3.
DR PROSITE; PS00014; ER_TARGET; UNKNOWN_1.
KW Signal.
FT SIGNAL 1 19 POTENTIAL.
FT CHAIN 20 421 CALRETICULIN.
SQ SEQUENCE 421 AA; 48822 MW; 172C664F59F41F93 CRC64;

Query Match 90.6%; Score 87; DB 5; Length 421;
Best Local Similarity 88.9%; Pred. No. 1.6e-05;
Matches 16; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 VIFNYKGNVLINKDIRC 18
DB 145 VIFNYKGNLTKKDIRC 162

RESULT 3
Q26268
ID Q26268 PRELIMINARY; PRT; 405 AA.
AC Q26268;
DT 01-NOV-1996 (TReMBLrel. 01, Created)
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
DT 01-JUN-2001 (TReMBLrel. 17, Last annotation update)
DE CALRETICULIN.
OS Aplysia californica (California sea hare).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Opisthobranchia; Anaspidae;
OC Aplysiidae; Aplysia.
OX NCBI_TaxID:6500;
RN [1]
RP SEQUENCE FROM N.A.
RA Kennedy T.E., Kuhl D., Barzilai A., Sweatt J.D., Kandel E.R.;
RT "Long-term sensitization training in Aplysia leads to an increase in
RT calreticulin, a major presynaptic calcium-binding protein.";
RL Neuron 9:1013-1024(1992).
DR EMBL; S51239; AAB24569.1; -;
DR InterPro; IPR000886; ER_target.
DR InterPro; IPR001580; Calreticulin.
DR Pfam; PF00262; calreticulin; 1.
DR PRINTS; PR00626; CALRETICULIN.
DR ProDom; PD001866; Calreticulin; 1.
DR PROSITE; PS00803; CALRETICULIN_1; 1.
DR PROSITE; PS00804; CALRETICULIN_2; 1.
DR PROSITE; PS00805; CALRETICULIN_REPEAT; 3.
DR PROSITE; PS00014; ER_TARGET; UNKNOWN_1.
SQ SEQUENCE 405 AA; 46738 MW; 14CAA201840D1D69 CRC64;

Query Match 89.6%; Score 86; DB 5; Length 405;
Best Local Similarity 83.3%; Pred. No. 2.1e-05;
Matches 15; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 VIFNYKGNVLINKDIRC 18
DB 142 VIFNYKGNLTKKDIRC 159

RESULT 4
Q16893
ID Q16893 PRELIMINARY; PRT; 410 AA.
AC Q16893;
DT 01-NOV-1996 (TReMBLrel. 01, Created)
DT 01-JAN-1999 (TReMBLrel. 09, Last sequence update)
DT 01-JUN-2001 (TReMBLrel. 17, Last annotation update)
DE CALRETICULIN.
GN CRT-1.
OS Amblyomma americanum.
OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Acari;
OC Parasitiformes; Ixodida; Ixodidae; Amblyomma.
OX NCBI_TaxID:6943;
RN [1]
RP SEQUENCE OF 49-410 FROM N.A.
RC TISSUE-SALIVARY GLANDS;
RA Jaworski D.C., Simmen F.A., Lamoreaux W.J., Coons L.B., Muller M.T.,
RA Needham G.R.;
RT "A secreted calreticulin protein in Ixodid tick (Amblyomma americanum)
RT saliva.";
RL J. Insect Physiol. 41:369-375(1995).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE-SALIVARY GLANDS;
RA Jaworski D.C.;
RL Submitted (MAR-1994) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE-SALIVARY GLANDS;
RA Pain-Thornton J.M., Jaworski D.C., Needham G.R.;
RL Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; U07708; AAC79094.1; -;
DR InterPro; IPR000886; ER_target.
DR InterPro; IPR001580; Calreticulin.
DR Pfam; PF00262; calreticulin; 1.
DR PRINTS; PR00626; CALRETICULIN.
DR ProDom; PD001866; Calreticulin; 1.
DR PROSITE; PS00803; CALRETICULIN_1; 1.
DR PROSITE; PS00805; CALRETICULIN_REPEAT; 3.
DR PROSITE; PS00014; ER_TARGET; UNKNOWN_1.
SQ SEQUENCE 410 AA; 47485 MW; 32CCB8750A17DC54 CRC64;

Query Match 88.5%; Score 85; DB 5; Length 410;
Best Local Similarity 88.9%; Pred. No. 3.1e-05;
Matches 16; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 VIFNYKGNVLINKDIRC 18
DB 145 VIFNYKGNLTKKDIRC 162

RESULT 5
Q9U916
ID Q9U916 PRELIMINARY; PRT; 406 AA.
AC Q9U916;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TReMBLrel. 17, Last annotation update)
DE CALRETICULIN.
GN CRC OR CG9429.
OS Drosophila melanogaster (Fruit fly).

OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=OREGON-R;
 RA Dodo K., Sakoyama Y., Gamo S.;
 RT "Drosophila melanogaster calreticulin for mRNA."
 RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AB000718; BAA85379.1; -
 DR FlyBase: FBgn0005585; Crc.
 DR InterPro: IPR001580; Calreticulin.
 DR InterPro: IPR000886; ER_target.
 DR Pfam: PF00262; calreticulin; 1.
 DR PRINTS: PR00626; CALRETICULIN.
 DR ProDom: PD001866; Calreticulin; 1.
 DR PROSITE: PS00803; CALRETICULIN_1; 1.
 DR PROSITE: PS00804; CALRETICULIN_2; 1.
 DR PROSITE: PS00805; CALRETICULIN_REPEAT; 3.
 DR PROSITE: PS00014; ER_TARGET; UNKNOWN_1.
 SQ SEQUENCE 406 AA; 46809 MW; 68BA49A6B81CC427 CRC64;

Query Match 82.3%; Score 79; DB 5; Length 406;
 Best Local Similarity 83.3%; Pred. No. 0.00026;
 Matches 15; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 QY 1 VIFNYGKGNVLKNDIRC 18
 DB 146 VIFSYGKNHLISKDIRC 163

RESULT 6
 Q98984
 ID Q98984 PRELIMINARY; PRT; 419 AA.
 AC Q98984
 DT 01-FEB-1997 (TREMBLrel. 02, Created)
 DT 01-FEB-1997 (TREMBLrel. 02, Last sequence update)
 DE 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
 DE CALRETICULIN.
 OS Rana rugosa (Frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; Rana.
 OX NCBI_TaxID=8410;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-96234004; PubMed-8654561;
 RA Yamamoto S., Nakamura M.;
 RT "Calnexin: its molecular cloning and expression in the liver of the
 RT frog, Rana rugosa."
 RL FEBS Lett. 387:27-32(1996).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Yamamoto S.;
 RT "Strong expression of the calreticulin gene in the liver of Rana
 RT rugosa Tadpoles."
 RL J. Exp. Zool. 0:0-0(1996).
 DR EMBL: D78589; BAA11425.1; -
 DR InterPro: IPR000886; ER_target.
 DR InterPro: IPR001580; Calreticulin.
 DR Pfam: PF00262; calreticulin; 1.
 DR PRINTS: PR00626; CALRETICULIN.
 DR ProDom: PD001866; Calreticulin; 1.
 DR PROSITE: PS00803; CALRETICULIN_1; 1.
 DR PROSITE: PS00804; CALRETICULIN_2; 1.
 DR PROSITE: PS00805; CALRETICULIN_REPEAT; 3.
 DR PROSITE: PS00014; ER_TARGET; UNKNOWN_1.
 SQ SEQUENCE 419 AA; 48658 MW; 2C857036769673BF CRC64;

Query Match 81.2%; Score 78; DB 13; Length 419;
 Best Local Similarity 88.2%; Pred. No. 0.00038;

Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 VIFNYGKGNVLKNDIRC 17
 DB 147 VIFNYGKGNLQINKDIR 163

RESULT 7
 Q9PUC1
 ID Q9PUC1 PRELIMINARY; PRT; 417 AA.
 AC Q9PUC1
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
 DE CALRETICULIN.
 OS Brachydanio rerio (zebrafish) (zebra danio).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
 OC Cypriniformes; Cyprinidae; Rasborinae; Danio.
 OX NCBI_TaxID=7955;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Rubinstein A.L., Lee D., Luo R., Henion P.D., Halpern M.E.;
 RT "Genes dependent on zebrafish cyclops function identified by AFLP
 RT Differential Gene Expression Screen."
 RL Genesis 0:0-0(1999).
 DR EMBL: AF195882; AAF13700.1; -
 DR InterPro: IPR000886; ER_target.
 DR InterPro: IPR001580; Calreticulin.
 DR Pfam: PF00262; calreticulin; 1.
 DR PRINTS: PR00626; CALRETICULIN.
 DR ProDom: PD001866; Calreticulin; 1.
 DR PROSITE: PS00803; CALRETICULIN_1; 1.
 DR PROSITE: PS00804; CALRETICULIN_2; 1.
 DR PROSITE: PS00805; CALRETICULIN_REPEAT; 3.
 DR PROSITE: PS00014; ER_TARGET; UNKNOWN_1.
 SQ SEQUENCE 417 AA; 48723 MW; 2000C5B4004699B6 CRC64;

Query Match 79.2%; Score 76; DB 13; Length 417;
 Best Local Similarity 77.8%; Pred. No. 0.00077;
 Matches 14; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 QY 1 VIFNYGKGNVLKNDIRC 18
 DB 146 VIFNYGKNHLKKDKC 163

RESULT 8
 O76961
 ID O76961 PRELIMINARY; PRT; 403 AA.
 AC O76961
 DT 01-NOV-1998 (TREMBLrel. 08, Created)
 DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
 DE CALRETICULIN PRECURSOR.
 GN CRT.
 OS Necator americanus.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Strongylida;
 OC Ancylostomatidae; Ancylostomatidae; Bunostominae; Necator.
 OX NCBI_TaxID=51031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Pritchard D.I., Brown A., McElroy P., Loukas A., Girdwood K.,
 RA Berry C., Fullkrug R., Beck E.;
 RT "Calreticulin is a hookworm allergen."
 RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AJ006790; CAA07254.1; -
 DR InterPro: IPR000886; ER_target.
 DR InterPro: IPR001580; Calreticulin.
 DR Pfam: PF00262; calreticulin; 1.
 DR PRINTS: PR00626; CALRETICULIN.
 DR ProDom: PD001866; Calreticulin; 1.

DR PROSITE; PS00803; CALRETICULIN_1; 1.
 DR PROSITE; PS00804; CALRETICULIN_2; 1.
 DR PROSITE; PS00805; CALRETICULIN_REPEAT; 3.
 DR PROSITE; PS00014; ER_TARGET; UNKNOWN_1.
 KW Signal; Allergen. 16 POTENTIAL.
 FT SIGNAL 1
 SQ SEQUENCE 403 AA; 46833 MW; 21F38B0515487B6F CRC64;

Query Match 77.1%; Score 74; DB 5; Length 403;
 Best Local Similarity 82.4%; Pred. No. 0.0015;
 Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 IFNYKGNVNLINKDIRC 18
 II:IIIIII:II:IIIIII

DB 143 IFSYKGNHLLIKKDIRC 159

RESULT 9
 Q91711 PRELIMINARY; PRT; 343 AA.

ID Q91711; 1998 (TREMBLrel. 05, Created)
 DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
 DE CALRETICULIN (FRAGMENT).

OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
 OC Xenopodidae; Xenopus.

NCBI_TaxID 8355;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE: BRAIN;

RX MEDLINE 93074997; PubMed 1445218;

RA Treves S., Zorzato F., Pozzan T.;

RT Identification of calreticulin isoforms in the central nervous

system.;

RL Blochm. J. 287:579-581(1992).

DR EMBL; X67598; CAA47867.1; -.

DR InterPro; IP001580; Calreticulin.

DR Pfam; PF00262; calreticulin; 1.

DR PRINTS; PR00626; CALRETICULIN.

DR PROXIM; PD001866; Calreticulin; 1.

DR PROSITE; PS00803; CALRETICULIN_1; 1.

DR PROSITE; PS00804; CALRETICULIN_2; 1.

FT NON_TER 1 343 343

SQ SEQUENCE 343 AA; 40105 MW; 3E7DDAFA33B91DE1 CRC64;

Query Match 76.0%; Score 73; DB 13; Length 343;
 Best Local Similarity 77.8%; Pred. No. 0.0018;
 Matches 14; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 VIFNYKGNVNLINKDIRC 18
 III:II:II:IIIIII

DB 118 VIFQYKKNLQINKDIRC 135

RESULT 10
 O18478 PRELIMINARY; PRT; 375 AA.

ID O18478; 1998 (TREMBLrel. 05, Created)

DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)

DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)

DE RAL-1 PROTEIN (FRAGMENT).

OS Litomosoides sigmodontis.

OC Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea;

OC Onchocercidae; Litomosoides.

NCBI_TaxID 42156;

RN SEQUENCE FROM N.A.
 RP MacLennan K., Hoffman W.H., Taylor D.W.;

RL Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.

DR EMBL; AJ001621; CAA04877.1; -.

DR InterPro; IP001580; Calreticulin.

DR Pfam; PF00262; calreticulin; 1.

DR PRINTS; PR00626; CALRETICULIN.

DR PRODOM; PD001866; Calreticulin; 1.

DR PROSITE; PS00803; CALRETICULIN_1; 1.

DR PROSITE; PS00804; CALRETICULIN_2; 1.

DR PROSITE; PS00805; CALRETICULIN_REPEAT; 3.

FT NON_TER 375 375

SQ SEQUENCE 375 AA; 43842 MW; 03F7642FBFF7A5B8 CRC64;

Query Match 76.0%; Score 73; DB 5; Length 375;
 Best Local Similarity 72.2%; Pred. No. 0.002;
 Matches 13; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 VIFNYKGNVNLINKDIRC 18
 III:IIII:II:IIII

DB 144 VIFHYKGRNHMKKDIRC 161

RESULT 11

O97372 PRELIMINARY; PRT; 387 AA.

ID O97372; 1999 (TREMBLrel. 10, Created)

DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)

DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)

DE CALRETICULIN PRECURSOR.

OS Dirofilaria immitis.

OC Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea;

OC Onchocercidae; Dirofilaria.

NCBI_TaxID 6287;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE 99094497; PubMed 9879888;

RA Tsuji N., Morales T.H., Ozols V.V., Carmody A.B., Chandrashekar R.;

RT Molecular characterization of a calcium-binding protein from the

filarial parasite Dirofilaria immitis.;

RL Mol. Biochem. Parasitol. 97:69-79(1998).

DR EMBL; AF052978; AAD03405.1; -.

DR InterPro; IP001580; Calreticulin.

DR Pfam; PF00262; calreticulin; 1.

DR PRINTS; PR00626; CALRETICULIN.

DR PRODOM; PD001866; Calreticulin; 1.

DR PROSITE; PS00803; CALRETICULIN_1; 1.

DR PROSITE; PS00804; CALRETICULIN_2; 1.

DR PROSITE; PS00805; CALRETICULIN_REPEAT; 3.

KW Signal.

FT SIGNAL 1 18 POTENTIAL.

FT CHAIN 19 387 CALRETICULIN.

SQ SEQUENCE 387 AA; 44941 MW; E7741BF6AFA5885 CRC64;

Query Match 76.0%; Score 73; DB 5; Length 387;
 Best Local Similarity 72.2%; Pred. No. 0.0021;
 Matches 13; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 VIFNYKGNVNLINKDIRC 18
 III:IIII:II:IIII

DB 144 VIFHYKGRNHMKKDIRC 161

RESULT 12

O91710 PRELIMINARY; PRT; 411 AA.

ID O91710; 1998 (TREMBLrel. 05, Created)

DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)

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Query Match          75.0%; Score 72; DB 5; Length 350;
Best Local Similarity 77.8%; Pred. No. 0.0027;
Matches 14; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 VIFNYGKGNVLINKDIRC 18
    |||||:| || ||| |
Db 99 VIFNYGKGNHLIKKDIPC 116

RESULT 14
O45034 PRELIMINARY; PRT; 396 AA.
AC O45034;
DT 01-JUN-1998 (TrEMBLrel. 05, Created)
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE CALRETICULIN.
OS Schistosoma japonicum (Blood fluke).
OC Eukaryota; Metazoa; Platyhelminthes; Rhabditophora; Neodermata;
OC Trematoda; Digenea; Strigeldida; Schistosomatoidea; Schistosomatidae;
OC Schistosoma.
OX NCBI_TaxID=6182;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PHILIPPINE (MINDORO);
RA Scott J.C.;
RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF044408; AAC00515.1; -
DR InterPro: IPR000886; ER_target.
DR InterPro: IPR001580; Calreticulin.
DR Pfam: PF00262; calreticulin; 1.
DR PRINTS: PR00626; CALRETICULIN.
DR ProDom: PD001866; Calreticulin; 1.
DR PROSITE: PS00803; CALRETICULIN_1; 1.
DR PROSITE: PS00804; CALRETICULIN_2; 1.
DR PROSITE: PS00805; CALRETICULIN_REPEAT; 2.
DR PROSITE: PS00014; ER_TARGET; UNKNOWN_1.
SQ SEQUENCE 396 AA; 45813 MW; C57394C6FB4CD77B CRC64;

Query Match          75.0%; Score 72; DB 5; Length 396;
Best Local Similarity 77.8%; Pred. No. 0.003;
Matches 14; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 VIFNYGKGNVLINKDIRC 18
    |||||:| || ||| |
Db 145 VIFNYGKGNHLIKKDIPC 162

RESULT 15
Q9U5G0 PRELIMINARY; PRT; 321 AA.
ID Q9U5G0
AC Q9U5G0;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE CALRETICULIN (FRAGMENT).
OS Eptatretus burgeri (Inshore hagfish).
OC Eukaryota; Metazoa; Chordata; Craniata; Hyperotretli; Myxiniformes;
OC Myxiniidae; Eptaretinae; Eptatretus.
OX NCBI_TaxID=7764;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LIVER;
RX MEDLINE=20063780; PubMed=10594174;
RA Kuraku S., Hoshiyama D., Katoh K., Suga H., Miyata T.;
RT "Monophyly of lampreys and hagfishes supported by nuclear DNA-coded
RT genes.";
RL J. Mol. Evol. 49:729-735(1999).
DR EMBL: AB025323; BAA88476.1; -.
DR InterPro: IPR000886; ER_target.
DR InterPro: IPR001580; Calreticulin.

```

DR pfam: PF00262; calreticulin; 1.
 DR PRINTS; PR00626; CALRETICULIN.
 DR ProDom; PD001866; Calreticulin; 1.
 DR PROSITE; PS00804; CALRETICULIN_2; 1.
 DR PROSITE; PS00805; CALRETICULIN_REPEAT; 3.
 DR PROSITE; PS00014; ER_TARGET; UNKNOWN_1.
 FT NON_TER 1
 SQ SEQUENCE 321 AA; 37367 MW; 6E8DFA98D42F7AEF CRC64;

Query Match 62.5%; Score 60; DB 13; Length 321;
 Best Local Similarity 61.1%; Pred. No. 0.18;
 Matches 11; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

OY 1 VIFNYKGNVLINKDIRC 18
 ||| |||| ||| :||
 Db 45 VILNSKGNHLIKKEVKC 62

Search completed: January 9, 2002, 15:03:29
 Job time: 271 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: January 9, 2002, 15:12:15 ; Search time 25.18 Seconds
(without alignments)
26.210 Million cell updates/sec

Title: US-09-828-000-6
Perfect score: 96
Sequence: 1 VIFNYKGNVLINKDIRC 18

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 100059 seqs, 36664827 residues

Total number of hits satisfying chosen parameters: 100059

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_39:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	96	100.0	400	1 CRT1_BOVIN	P52193 bos taurus
2	96	100.0	416	1 CRTC_MOUSE	P14211 mus musculus
3	96	100.0	416	1 CRTC_RAT	P18418 rattus norv
4	96	100.0	417	1 CRTC_HUMAN	P27797 homo sapien
5	96	100.0	418	1 CRTC_RABIT	P15253 oryctolagus
6	96	100.0	421	1 CRT2_BOVIN	P42918 bos taurus
7	79	82.3	406	1 CRTC_DROME	P29413 drosophila
8	72	75.0	393	1 CRTC_SCHMA	Q06814 schistosoma
9	66	68.8	388	1 RALI_ONCVO	P11012 onchocerca
10	64	66.7	395	1 CRTC_CAEEL	P27798 caenorhabdi
11	61	63.5	420	1 CRTC_CHLRE	Q9std3 chlamydomon
12	59	61.5	424	1 CRTC_DICDI	Q23858 dictyosteli
13	53	55.2	401	1 CRTC_EUGGR	Q9zdv3 euglena gra
14	53	55.2	416	1 CRTC_BETVU	O81919 beta vulgar
15	52	54.2	424	1 CRT3_ARATH	O04153 arabidopsis
16	51	53.1	725	1 NCA2_MOUSE	P13594 mus musculus
17	51	53.1	761	1 NCA2_HUMAN	P13592 homo sapien
18	51	53.1	848	1 NCA1_HUMAN	P13591 homo sapien
19	51	53.1	853	1 NCA1_BOVIN	P13836 bos taurus
20	51	53.1	858	1 NCA1_RAT	P13596 rattus norv
21	51	53.1	1091	1 NCA1_CHICK	P13590 gallus gall
22	51	53.1	1115	1 NCA1_MOUSE	P13595 mus musculus
23	48	50.0	421	1 CRTC_PRUAR	Q9xf98 prunus arne
24	48	50.0	424	1 CRT2_ARATH	Q38858 arabidopsis
25	48	50.0	463	1 VSHA_CHICK	Q90578 gallus gall
26	47	49.0	1088	1 NCA1_XENLA	P16170 xenopus lae
27	47	49.0	1092	1 NCA2_XENLA	P36335 xenopus lae
28	44	45.8	417	1 PGK_METJA	Q58058 methanococc
29	44	45.8	420	1 CRTC_MAIZE	Q9sp22 zea mays (m
30	44	45.8	424	1 CRTC_ORISA	Q9sly8 oryza sativ
31	44	45.8	425	1 CRT1_ARATH	O04151 arabidopsis
32	44	45.8	496	1 CHK1_SCHPO	P34208 schizosacch
33	43	44.8	327	1 RPOA_UREPA	Q9pqn4 ureaplasma

Query Match 100.0%; Score 96; DB 1; Length 400;
Best Local Similarity 100.0%; Pred. No. 1.3e-07;

RESULT 1

ID	CRT1_BOVIN	STANDARD;	PRT;	400 AA.
AT	P52193;			
DT	01-OCT-1996 (Rel. 34, Created)			
DT	01-OCT-1996 (Rel. 34, Last sequence update)			
DT	01-OCT-1996 (Rel. 34, Last annotation update)			
DE	CALRETICULIN, BRAIN ISOFORM 1 (CRP55) (CALREGULIN) (HACBP).			
OS	Bos taurus (Bovine).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;			
OC	Bovidae; Bovinae; Bos.			
OX	NCBI_TaxID=9913;			
RN	[1]			
RP	SEQUENCE.			
RC	TISSUE=Brain;			
RC	MEDLINE=94183174; PubMed=8135753;			
RA	Matsuoka K., Seta K., Yamakawa Y., Okuyama T., Shinoda T., Isobe T.;			
RT	"Covalent structure of bovine brain calreticulin.";			
RL	Biochem. J. 298:435-442(1994).			
CC	-!- FUNCTION: THIS PROTEIN BINDS CALCIUM. THERE ARE BOTH HIGH AND LOW AFFINITY CALCIUM-BINDING SITES.			
CC	-!- SUBUNIT: MONOMER.			
CC	-!- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM LUMEN.			
CC	-!- SIMILARITY: BELONGS TO THE CALRETICULIN FAMILY.			
DR	InterPro: IPR001580; Calreticulin.			
DR	InterPro: IPR000886; ER_target.			
DR	Pfam: PF00262; calreticulin; 1.			
DR	PRINTS: PR00626; CALRETICULIN.			
DR	ProDom: PD001866; Calreticulin; 1.			
DR	PROSITE: PS00014; ER_TARGET; 1.			
DR	PROSITE: PS00803; CALRETICULIN_1; 1.			
DR	PROSITE: PS00804; CALRETICULIN_2; 1.			
DR	PROSITE: PS00805; CALRETICULIN_REPEAT; 3.			
KW	Endoplasmic reticulum; Calcium-binding; Repeat; Glycoprotein.			
FT	DOMAIN 1 180 N-DOMAIN.			
FT	DOMAIN 181 291 P-DOMAIN.			
FT	DOMAIN 292 400 C-DOMAIN.			
FT	DOMAIN 174 238 4 X APPROXIMATE REPEATS.			
FT	REPEAT 174 185 1-1.			
FT	REPEAT 193 204 1-2.			
FT	REPEAT 210 221 1-3.			
FT	REPEAT 227 238 1-4.			
FT	REPEAT 242 280 3 X APPROXIMATE REPEATS.			
FT	REPEAT 242 252 2-1.			
FT	REPEAT 256 266 2-2.			
FT	REPEAT 270 280 2-3.			
FT	DOMAIN 334 390 ASP/GLU/LYS-RICH.			
FT	DISULFID 120 146			
FT	CARBOHYD 162 162			
FT	SITE 397 400 N-LINKED (GLCNAC. . .).			
FT	SEQUENCE 400 AA; 46381 MW; 7D4B68DFC689EEF1 CRC64;			
SQ				

ALIGNMENTS

34	43	44.8	415	1 CRTC_RICCO	P93508 ricinus com
35	43	44.8	435	1 KIN3_YEAST	P22209 saccharomyc
36	42	43.8	222	1 GIDB_TREPA	O66106 treponema p
37	42	43.8	348	1 AFUC_ACTPL	O57293 actinobacil
38	42	43.8	488	1 YGM9_YEAST	O01163 saccharomyc
39	42	43.8	732	1 EF2_PYRAB	O9v128 pyrococcus
40	42	43.8	732	1 EF2_PYRHO	O59521 pyrococcus
41	42	43.8	732	1 EF2_PYRHO	P29050 pyrococcus
42	42	43.8	803	1 SUSY_ALNGL	P49034 alnus glut
43	41	42.7	238	1 Y037_METJA	O60344 methanococc
44	41	42.7	284	1 HPRT_SCHMA	P09383 schistosoma
45	41	42.7	286	1 RIPI_WOMCH	P16094 momordica c

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VIFNYGKNVLINKDIRC 18
 DB 129 VIFNYGKNVLINKDIRC 146

RESULT 2
 CRTCL_MOUSE STANDARD; PRT; 416 AA.
 AC PL4211;
 DT 01-JAN-1990 (Rel. 13, Created)
 DT 01-JAN-1990 (Rel. 13, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DR CALRETICULIN PRECURSOR (CRP55) (CALREGULIN) (HACBP) (ERP60).
 GN CALR.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID:10090;
 RN [1]
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 18-48 AND 129-161.
 RC STRAIN BALB/C; TISSUE=Liver;
 RX MEDLINE 90059955; PubMed:2583110;
 RA Smith M.J., Koch G.L.E.;
 RT "Multiple zones in the sequence of calreticulin (CRP55, calregulin,
 RT HACBP), a major calcium binding ER/SR protein.";
 RL EMBO J. 8:3581-3586(1989).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE 93013037; PubMed 1398135;
 RA Mazzarella R.A., Gold P., Cunningham M., Green M.;
 RT "Determination of the sequence of an expressible cDNA clone encoding
 RT Exp60/calregulin by the use of a novel nested set method.";
 RL Gene 120:217-225(1992).
 RN [3]
 RP SEQUENCE OF 18-38.
 RC TISSUE=Fibroblast;
 RX MEDLINE 95009907; PubMed 7523108;
 RA Merrick R.A., Patterson R.M., Wichter L.L., He C., Selkirk J.K.;
 RT "Separation and sequencing of familial and novel murine proteins
 RT using preparative two-dimensional gel electrophoresis.";
 RL Electrophoresis 15:735-745(1994).
 RN [4]
 RP FUNCTION: THIS PROTEIN BINDS CALCIUM. THERE ARE BOTH HIGH AND
 RP LOW AFFINITY CALCIUM-BINDING SITES.
 CC -1 SURUNIT: MONOMER (BY SIMILARITY).
 CC -1 SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM LUMEN.
 CC -1 SIMILARITY: BELONGS TO THE CALRETICULIN FAMILY.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; X14926; CAA33053.1; -;
 DR EMBL; M92988; AAA37569.1; -;
 DR PIR; S06763; S06763.
 DR PIR; JC1444; JC1444.
 DR SWISS-2DPAGE; PL4211; MOUSE.
 DR MGI; 88252; Calr.
 DR InterPro; IPR001580; Calreticulin.
 DR InterPro; IPR000886; ER_target.
 DR Pfam; PF00262; calreticulin_1.
 DR PRINTS; PR00626; CALRETICULIN.
 DR ProDom; PD001866; Calreticulin.
 DR PROSITE; PS00014; ER_TARGET; 1.
 DR PROSITE; PS00803; CALRETICULIN_1; 1.
 DR PROSITE; PS00804; CALRETICULIN_2; 1.
 DR PROSITE; PS00805; CALRETICULIN_REPEAT; 3.
 KW Endoplasmic reticulum; Calcium-binding; Repeat; Signal.

FT SIGNAL 1 17
 FT CHAIN 18 416
 FT DOMAIN 18 197
 FT DOMAIN 198 308
 FT DOMAIN 309 416
 FT DOMAIN 191 255
 FT REPEAT 191 202
 FT REPEAT 210 221
 FT REPEAT 227 238
 FT REPEAT 244 255
 FT DOMAIN 259 297
 FT REPEAT 259 269
 FT REPEAT 273 283
 FT REPEAT 287 297
 FT DOMAIN 351 407
 FT DISULFID 137 163
 FT SITE 413 416
 SQ SEQUENCE 416 AA; 47994 MW; 24C03B00913408D8 CRC64;

Query Match 100.0%; Score 96; DB 1; Length 416;
 Best Local Similarity 100.0%; Pred. No. 1.4e-07;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VIFNYGKNVLINKDIRC 18
 DB 146 VIFNYGKNVLINKDIRC 163

RESULT 3
 CRTCL_RAT STANDARD; PRT; 416 AA.
 AC P18418; P10452;
 DT 01-MAR-1989 (Rel. 10, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE CALRETICULIN PRECURSOR (CRP55) (CALREGULIN) (HACBP) (ERP60) (CALBP)
 DE (CALCIUM-BINDING PROTEIN 3) (CABP3).
 GN CALR.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID:10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-SPRAGUE-DAWLEY; TISSUE=Brain cortex;
 RX MEDLINE-90370496; PubMed:2395661;
 RA Murthy K.K., Banville D., Srikant C.B., Carrier F., Bell A.,
 RA Holmes C., Patel Y.C.;
 RT "Structural homology between the rat calreticulin gene product and
 RT the Onchocerca volvulus antigen Rai-1.";
 RL Nucleic Acids Res. 18:4933-4933(1990).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-SPRAGUE-DAWLEY;
 RX MEDLINE-93202172; PubMed-8453984;
 RA Nakanura M., Moriya M., Baba T., Michikawa Y., Yamanobe T., Arai K.,
 RA Okinaga S., Kobayashi T.;
 RT "An endoplasmic reticulum protein, calreticulin, is transported into
 RT the acrosome of rat sperm.";
 RL Exp. Cell Res. 205:101-110(1993).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN-SPRAGUE-DAWLEY; TISSUE=Liver;
 RX MEDLINE-95181573; PubMed:7876339;
 RA Soennichsen B., Fuelekruug J., van Nguyen P., Diekmann W.,
 RA Robinson D.G., Mieskes G.;
 RT "Retention and retrieval: both mechanisms cooperate to maintain
 RT calreticulin in the endoplasmic reticulum.";
 RL J. Cell Sci. 107:2705-2717(1994).
 RN [4]
 RP SEQUENCE OF 270-358 FROM N.A.
 RC STRAIN-SPRAGUE-DAWLEY;

RA Lone Y.C., Bailly A., Latruffe N.;
RL Submitted (DEC-1988) to the EMBL/GenBank/DDBJ databases.
RN [5]
RX SEQUENCE OF 18-29.
RA MEDLINE=91054414; PubMed=2241926;
RA Treves S., de Mattei M., Lanfredi M., Villa A., Green N.M.,
RA MacLennan D.H., Meldolesi J., Pozzan T.;
RA "Calreticulin is a candidate for a calsequestrin-like function in
RT Ca2(+)-storage compartments (calciosomes) of liver and brain.";
RL Biochem. J. 271:473-480(1990).
RN [6]
RP SEQUENCE OF 18-32.
RC STRAIN=SPRAGUE-DAWLEY; TISSUE=Testis;
RX MEDLINE=92360010; PubMed=1497655;
RA Nakamura M., Michikawa Y., Baba T., Okinaga S., Arai K.;
RA "Calreticulin is present in the acrosome of spermatids of rat
RT testis";
RL Biochem. Biophys. Res. Commun. 186:668-673(1992).
RN [7]
RP SEQUENCE OF 18-32.
RC STRAIN=LEC; TISSUE=Liver;
RX MEDLINE=94072621; PubMed=8251535;
RA Yokoi T., Nagayama S., Kajiwara R., Kawaguchi Y., Horiuchi R.,
RA Kamataki T.;
RT "Identification of protein disulfide isomerase and calreticulin as
RT autoimmune antigens in LEC strain of rats.";
RL Biochim. Biophys. Acta 1158:339-344(1993).
CC -!- FUNCTION: THIS PROTEIN BINDS CALCIUM. THERE ARE BOTH HIGH AND
CC LOW AFFINITY CALCIUM-BINDING SITES.
CC -!- SUBUNIT: MONOMER (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM LUMEN.
CC -!- SIMILARITY: BELONGS TO THE CALRETICULIN FAMILY.
CC -!- CAUTION: WAS ORIGINALLY (REF.2) THOUGHT TO BE D-BETA-
CC HYDROXYBUTYRATE DEHYDROGENASE.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; D78308; BAA11345.1; -;
DR EMBL; X53363; CAA37446.1; -;
DR EMBL; X13702; CAA31987.1; -;
DR EMBL; X79327; CAA55890.1; -;
DR PIR; S04867; S04867.
DR PIR; S13045; S13045.
DR PIR; A49176; A49176.
DR PIR; S45036; S45036.
DR PIR; JH0819; JH0819.
DR InterPro; IPR001580; Calreticulin.
DR InterPro; IPR000886; ER target.
DR Pfam; PF00262; calreticulin; 1.
DR PRINTS; PR00626; CALRETICULIN.
DR PRODOM; PD001866; Calreticulin; 1.
DR PROSITE; PS00014; ER_TARGET; 1.
DR PROSITE; PS00803; CALRETICULIN_1; 1.
DR PROSITE; PS00804; CALRETICULIN_2; 1.
DR PROSITE; PS00805; CALRETICULIN_REPEAT; 3.
KW Endoplasmic reticulum; Calcium-binding; Repeat; Signal.
FT SIGNAL 1 17
FT CHAIN 18 416 CALRETICULIN.
FT DOMAIN 18 197 N-DOMAIN.
FT DOMAIN 198 308 P-DOMAIN.
FT DOMAIN 309 416 C-DOMAIN.
FT DOMAIN 191 255 4 X APPROXIMATE REPEATS.
FT REPEAT 191 202 1-1.
FT REPEAT 210 221 1-2.
FT REPEAT 227 238 1-3.
FT REPEAT 244 255 1-4.

FT DOMAIN 259 297 3 X APPROXIMATE REPEATS.
FT REPEAT 259 269 2-1.
FT REPEAT 273 283 2-2.
FT REPEAT 287 297 2-3.
FT DOMAIN 351 407 ASP/GLU/LYS-RICH.
FT DISULFID 137 163 BY SIMILARITY.
FT SITE 413 416 PREVENT SECRETION FROM ER.
SQ SEQUENCE 416 AA; 47995 MW; 2E6713CED31A2970 CRC64;

Query Match 100.0%; Score 96; DB 1; Length 416;
Best Local Similarity 100.0%; Pred. No. 1.4e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VIFNYKGNVLINKDIRC 18
Db 146 VIFNYKGNVLINKDIRC 163
|||||

RESULT 4
ID CRTC_HUMAN STANDARD; PRT; 417 AA.
AC P27797;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE CALRETICULIN PRECURSOR (CRP55) (CALREGULIN) (HACBP) (ERP60) (52 KDA
DE RIBONUCLEOPROTEIN AUTOANTIGEN RO/SS-A).
GN CALR OR CRTC.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
ON NCBI_TaxID=9606;
RX [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92013129; PubMed=1919005;
RA Rokeach L.A., Haselby J.A., Melloy F.F., Smeenk R.J., Unnasch T.R.,
RA Greene B.M., Hoch S.O.;
RT "Characterization of the autoantigen calreticulin.";
RL J. Immunol. 147:3031-3039(1991).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=90237213; PubMed=2332496;
RA McCaulliffe D.P., Lux F.A., Lieu T.S., Sanz I., Hanke J., Newkirk M.M.,
RA Bachinski L.L., Itoh Y., Siciliano M.J., Reichlin M., Sontheimer R.D.,
RA Capra J.D.;
RT "Molecular cloning, expression, and chromosome 19 localization of a
RT human Ro/SS-A autoantigen.";
RL J. Clin. Invest. 85:1379-1391(1990).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=92129342; PubMed=1733953;
RA McCaulliffe D.P., Yang Y.S., Wilson J., Sontheimer R.D., Capra J.D.;
RT "The 5'-flanking region of the human calreticulin gene shares
RT homology with the human GRP78, GRP94, and protein disulfide isomerase
RT promoters.";
RL J. Biol. Chem. 267:2557-2562(1992).
RN [4]
RP SEQUENCE FROM N.A.
RA Lamerdin J., McCreedy P., Stilwagen S., Ramirez M., Carrano A.;
RL Submitted (MAR-1997) to the EMBL/GenBank/DDBJ databases.
RN [5]
RP SEQUENCE OF 18-36.
RX MEDLINE=92002034; PubMed=1911778;
RA Rojiani M.V., Finlay B.B., Gray V., Dedhar S.;
RT "In vitro interaction of a polypeptide homologous to human Ro/SS-A
RT antigen (calreticulin) with a highly conserved amino acid sequence in
RT the cytoplasmic domain of integrin alpha subunits.";
RL Biochemistry 30:9859-9866(1991).
RN [6]
RP SEQUENCE OF 18-32.
RX MEDLINE=90380058; PubMed=2400400;
RA Krause K.H., Simmerman H.K.B., Jones L.R., Campbell K.P.;

*Sequence similarity of calreticulin with a Ca2(+)-binding protein that co-purifies with an Ins(1,4,5)P3-sensitive Ca2+ store in HL-60 cells.";
 Biochem. J. 270:545-548(1990).

[7]

RN SEQUENCE OF 18-28.

RC TISSUE Liver;

RX MEDLINE-93162045; PubMed 1286669;

RA Hochstrasser D.F., Frutiger S., Paquet N., Bairoch A., Ravier F.,

RA Pasquali C., Sanchez J.-C., Tissot J.-D., Bjellqvist B., Vargas R.,

RA Appel R.D., Hughes G.J.;

*Human liver protein map: a reference database established by

microsequencing and gel comparison.";

Electrophoresis 13:992-1001(1992).

[8]

PARTIAL SEQUENCE OF 25-34; 56-62; 208-221 AND 273-278.

RC TISSUE-Keratinocytes;

RX MEDLINE-93162043; PubMed 1286667;

RA Ramnathan H.H., Van Damme J., Puype M., Gessner B., Celis J.E.,

RA Vandekerckhove J.;

*Microsequences of 145 proteins recorded in the two-dimensional gel

protein database of normal human epidermal keratinocytes.";

Electrophoresis 13:960-969(1992).

[9]

SEQUENCE OF 18-26.

RC TISSUE-Colon carcinoma;

RX MEDLINE 97295306; PubMed 9150948;

RA Ji H., Reid G.E., Moritz R.L., Eddes J.S., Burgess A.W., Simpson R.J.;

*A two-dimensional gel database of human colon carcinoma proteins.";

Electrophoresis 18:605-613(1997).

CC 1- FUNCTION: THIS PROTEIN BINDS CALCIUM. THERE ARE BOTH HIGH AND

LOW AFFINITY CALCIUM-BINDING SITES.

CC 1- SUBUNIT: MONOMER (BY SIMILARITY).

CC 1- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM LUMEN.

CC 1- SIMILARITY: BELONGS TO THE CALRETICULIN FAMILY.

CC 1- CAUTION: WAS ORIGINALLY (REF.2) THOUGHT TO BE THE RO AUTOANTIGEN.

CC

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CC

DR EMBL; M84739; AAA51916.1; -

DR EMBL; M32294; AAA36582.1; -

DR EMBL; AD000092; AAB51176.1; -

DR PIR; A37047; A37047.

DR PIR; S11475; S11475.

DR PIR; A42330; A42330.

DR PIR; A46452; A46452.

DR SWISS-2DPAGE; P27797; HUMAN.

DR Aarbus/Ghent-2DPAGE; 9401; IEF.

DR HSC-2DPAGE; P27797; HUMAN.

DR MIM; 109091; -

DR InterPro; IPR001580; Calreticulin.

DR InterPro; IPR000886; ER-target.

DR Pfam; PF00262; calreticulin; 1.

DR PRINTS; PR00626; CALRETICULIN.

DR ProDom; PD001866; Calreticulin; 1.

DR PROSITE; PS00014; ER-TARGET; 1.

DR PROSITE; PS00803; CALRETICULIN; 1.

DR PROSITE; PS00804; CALRETICULIN; 2; 1.

DR PROSITE; PS00805; CALRETICULIN-REPEAT; 3.

KW Endoplasmic reticulum; Calcium-binding; Repeat; Signal.

FT SIGNAL 1 17

FT CHAIN 18 417

FT DOMAIN 18 197

FT DOMAIN 198 308

FT DOMAIN 309 417

FT DOMAIN 191 255

FT REPEAT 191 202

FT REPEAT 191 202

FT REPEAT 210 221 1-2.
 FT REPEAT 227 238 1-3.
 FT REPEAT 244 255 1-4.
 FT DOMAIN 259 297 3 X APPROXIMATE REPEATS.
 FT REPEAT 259 269 2-1.
 FT REPEAT 273 283 2-2.
 FT REPEAT 287 297 2-3.
 FT DOMAIN 351 408 ASP/GLU/LYS-RICH.
 FT DISULFID 137 163 BY SIMILARITY.
 FT SITE 414 417 PREVENT SECRETION FROM ER.
 FT CONFLICT 35 35 MISSING (IN REF. 3).
 SQ SEQUENCE 417 AA; 48141 MW; BC37C3C0F1054FB2 CRC64;

Query Match 100.0%; Score 96; DB 1; Length 417;
 Best Local Similarity 100.0%; Pred. NO. 1.4e-07;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VIFNYKGNVINKDIRC 18

Db 146 VIFNYKGNVINKDIRC 163

RESULT 5

CRTC_RABIT

ID CRTC_RABIT STANDARD; PRT; 418 AA.

AC P15253;

DT 01-APR-1990 (Rel. 14, Created)

DT 01-APR-1990 (Rel. 14, Last sequence update)

DT 01-OCT-1996 (Rel. 34, Last annotation update)

DE CALRETICULIN PRECURSOR (CRP55) (CALREGULIN) (HACBP) (ERP60).

GN CALR.

OS Oryctolagus cuniculus (Rabbit).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.

OX NCBI_TaxID:9986;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE-Slow-twitch skeletal muscle;

RX MEDLINE-90094320; PubMed-2600080;

RA Fliegel L., Burns K., MacLennan D.H., Reithmeier R.A.F., Michalak M.;

RT "Molecular cloning of the high affinity calcium-binding protein

(calreticulin) of skeletal muscle sarcoplasmic reticulum.";

RL J. Biol. Chem. 264:21522-21528(1989).

RN [2]

RP SEQUENCE FROM N.A.

RC TISSUE-Fast-twitch skeletal muscle;

RX MEDLINE-91282795; PubMed-2059224;

RA Fliegel L., Michalak M.;

RT "Fast-twitch and slow-twitch skeletal muscles express the same

isoform of calreticulin.";

RL Biochem. Biophys. Res. Commun. 177:979-984(1991).

RN [3]

RP SEQUENCE OF 18-36.

RX MEDLINE-91054414; PubMed-2241926;

RA Treves S., de Mattel M., Lanfredi M., Villa A., Green N.M.,

RA MacLennan D.H., Meldolesi J., Pozzan T.;

RT "Calreticulin is a candidate for a calsequestrin-like function in

Ca2(+)-storage compartments (calciosomes) of liver and brain.";

RL Biochem. J. 271:473-480(1990).

RN [4]

RP SEQUENCE OF 18-46.

RX MEDLINE-91201375; PubMed-2016321;

RA Milner R.E., Baksh S., Shemanko C., Carpenter M.R., Smillie L.,

RA Vance J.E., Opas M., Michalak M.;

RT "Calreticulin, and not calsequestrin, is the major calcium binding

protein of smooth muscle sarcoplasmic reticulum and liver endoplasmic

reticulum.";

RL J. Biol. Chem. 266:7155-7165(1991).

RN [5]

RP PARTIAL SEQUENCE.

RC TISSUE-Lung;

RX MEDLINE-92002038; PubMed-1911780;

RA Guan S., Fallick A.M., Williams D.E., Cashman J.R.:
 RT "Evidence for complex formation between rabbit lung flavin-containing
 RL monooxygenase and calreticulin.";
 CC Biochemistry 30:9892-9900(1991).
 CC -!- FUNCTION: THIS PROTEIN BINDS CALCIUM. THERE ARE BOTH HIGH AND
 CC LOW AFFINITY CALCIUM-BINDING SITES.
 CC -!- SUBUNIT: MONOMER (BY SIMILARITY).
 CC -!- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM LUMEN.
 CC -!- SIMILARITY: BELONGS TO THE CALRETICULIN FAMILY.
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 CC -----
 DR EMBL: J05138; AAA31188.1; -;
 DR PIR: A34154; A34154.
 DR PIR: C33208; C33208.
 DR PIR: D33208; D33208.
 DR PIR: E33208; E33208.
 DR PIR: F33208; F33208.
 DR PIR: S13046; S13046.
 DR PIR: S13047; S13047.
 DR InterPro: IPR001580; Calreticulin.
 DR InterPro: IPR000886; ER target.
 DR Pfam: PF00262; calreticulin; 1.
 DR PRINTS: PR00626; CALRETICULIN.
 DR PRODOM: PD001866; Calreticulin; 1.
 DR PROSITE: PS000014; ER_TARGET; 1.
 DR PROSITE: PS00803; CALRETICULIN_1; 1.
 DR PROSITE: PS00804; CALRETICULIN_2; 1.
 DR PROSITE: PS00805; CALRETICULIN_REPEAT; 3.
 KW Endoplasmic reticulum; Calcium-binding; Repeat; Signal.
 FT SIGNAL 1 17
 FT CHAIN 18 418 CALRETICULIN.
 FT DOMAIN 18 197 N-DOMAIN.
 FT DOMAIN 198 308 P-DOMAIN.
 FT DOMAIN 309 418 C-DOMAIN.
 FT DOMAIN 191 -255 4 X APPROXIMATE REPEATS.
 FT REPEAT 191 202 1-1.
 FT REPEAT 210 221 1-2.
 FT REPEAT 227 238 1-3.
 FT REPEAT 244 255 1-4.
 FT DOMAIN 259 297 3 X APPROXIMATE REPEATS.
 FT REPEAT 259 269 2-1.
 FT REPEAT 273 283 2-2.
 FT REPEAT 287 297 2-3.
 FT DOMAIN 351 408 ASP/GLU/LYS-RICH.
 FT DISULFID 137 163 BY SIMILARITY.
 FT SITE 415 418 PREVENT SECRETION FROM ER.
 FT VARIANT 35 35 E -> D.
 FT CONFLICT 90 90 P -> T (IN REF. 5).
 SQ SEQUENCE 418 AA; 48275 MW; B6082B689DC763A6 CRC64;

Query Match 100.0%; Score 96; DB 1; Length 418;
 Best Local Similarity 100.0%; Pred. No. 1.4e-07;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VIFNYKGNVLINKDIRC 18
 |||||
 Db 146 VIFNYKGNVLINKDIRC 163
 |||||

RESULT 6
 ID CRT2_BOVIN STANDARD; PRT; 421 AA.
 AC P42918;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)

DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE CALRETICULIN, BRAIN ISOFORM 2 PRECURSOR (CRP55) (CALREGULIN) (HACBP).
 OS Bos taurus (Bovine).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 CC Bovidae; Bovinae; Bos.
 CC NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=93385184; PubMed=8373827;
 RA Liu N., Fine R.E., Johnson R.J.;
 RT "Comparison of cDNAs from bovine brain coding for two isoforms of
 RT calreticulin.";
 RL Biochem. Biophys. Acta 1202:70-76(1993).
 CC -!- FUNCTION: THIS PROTEIN BINDS CALCIUM. THERE ARE BOTH HIGH AND
 CC LOW AFFINITY CALCIUM-BINDING SITES.
 CC -!- SUBUNIT: MONOMER (BY SIMILARITY).
 CC -!- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM LUMEN.
 CC -!- SIMILARITY: BELONGS TO THE CALRETICULIN FAMILY.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: L13462; AAC37307.1; -;
 DR InterPro: IPR001580; Calreticulin.
 DR InterPro: IPR000886; ER target.
 DR Pfam: PF00262; calreticulin; 1.
 DR PRINTS: PR00626; CALRETICULIN.
 DR PRODOM: PD001866; Calreticulin; 1.
 DR PROSITE: PS000014; ER_TARGET; 1.
 DR PROSITE: PS00803; CALRETICULIN_1; 1.
 DR PROSITE: PS00804; CALRETICULIN_2; 1.
 DR PROSITE: PS00805; CALRETICULIN_REPEAT; 3.
 KW Endoplasmic reticulum; Calcium-binding; Repeat; Signal.
 FT SIGNAL 1 34 POTENTIAL.
 FT CHAIN 35 421 CALRETICULIN, BRAIN ISOFORM 2.
 FT DOMAIN 35 201 N-DOMAIN.
 FT DOMAIN 202 312 P-DOMAIN.
 FT DOMAIN 313 421 C-DOMAIN.
 FT DOMAIN 195 259 4 X APPROXIMATE REPEATS.
 FT REPEAT 195 206 1-1.
 FT REPEAT 214 225 1-2.
 FT REPEAT 231 242 1-3.
 FT REPEAT 248 259 1-4.
 FT DOMAIN 263 301 3 X APPROXIMATE REPEATS.
 FT REPEAT 263 273 2-1.
 FT REPEAT 277 287 2-2.
 FT REPEAT 291 301 2-3.
 FT DOMAIN 366 411 ASP/GLU/LYS-RICH.
 FT DISULFID 141 167 BY SIMILARITY.
 FT CARBOHYD 183 183 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT SITE 418 421 PREVENT SECRETION FROM ER.
 SQ SEQUENCE 421 AA; 48812 MW; 0257E959F71528BC CRC64;

Query Match 100.0%; Score 96; DB 1; Length 421;
 Best Local Similarity 100.0%; Pred. No. 1.4e-07;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VIFNYKGNVLINKDIRC 18
 |||||
 Db 150 VIFNYKGNVLINKDIRC 167
 |||||

RESULT 7
 ID CRTC_DROME STANDARD; PRT; 406 AA.

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AC DT 01-APR-1993 (Rel. 25, Created)
DT 01-OCT-1993 (Rel. 27, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE CALRETICULIN PRECURSOR (CRP55) (CALRETCULIN) (HACBP).
GN CRC OR CG9429.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephyroidae; Drosophilidae; Drosophila.
OX NCBI_TaxID: 7227;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE 93208374; PubMed 1296819;
NA Smith M.J.;
RT "Nucleotide sequence of a Drosophila melanogaster gene encoding a
RL calreticulin homologue";
RL DNA Seq. 3:247-250(1992).
RN [2]
RP SEQUENCE FROM N.A.
KC STRAIN BERKELEY;
RX MEDLINE 20196006; PubMed 10731132;
RA Adams M.D., Colnicker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.C., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blake J.R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G.G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballou R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Bonos P.V., Borman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downs M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Fowler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalili M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattel B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.M., Nelson K.A., Nixon K., Nusskern D.R., Pacle J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RL Science 287:2185-2195(2000).
RN [3]
RP SEQUENCE OF 91-124 AND 182-220.
RX MEDLINE 90307981; PubMed 2365822;
RA McCaulliffe D.P., Zappi E., Lieu T.S., Michalak M., Sontheimer R.D.,
RA Capra J.D.;
RT highly homologous with onchocercal RAL-1 antigen and an aplasia
RT 'memory molecule';
RL J. Clin. Invest. 86:332-335(1990).
CC -!- FUNCTION: THIS PROTEIN BINDS CALCIUM. THERE ARE BOTH HIGH AND
CC -!- AFFINITY CALCIUM-BINDING SITES.
CC -!- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM LUMEN.
CC -!- SIMILARITY: BELONGS TO THE CALRETICULIN FAMILY.

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EMBL; X64461; CAA45791.1; -
EMBL; AE003683; AAF54416.1; -
DR PIR; A37158; A37158.
DR FlyBase; FBgn0005585; Crc.
DR InterPro; IPR001580; Calreticulin.
DR InterPro; IPR000886; ER_target.
DR Pfam; PF00262; calreticulin; 1.
DR PRINTS; PR00626; CALRETICULIN.
DR ProDom; PD001866; Calreticulin; 1.
DR PROSITE; PS00014; ER_TARGET; 1.
DR PROSITE; PS00803; CALRETICULIN_1; 1.
DR PROSITE; PS00804; CALRETICULIN_2; 1.
DR PROSITE; PS00805; CALRETICULIN_REPEAT; 3.
KW Endoplasmic reticulum; Calcium-binding; Repeat; Signal.
FT SIGNAL 1 17 POTENTIAL.
FT CHAIN 18 406 CALRETICULIN.
FT CONFLICT 107 107 G -> A (IN REF. 3).
FT CONFLICT 184 184 V -> L (IN REF. 3).
SQ SEQUENCE 406 AA; 46808 MW; 65D72C69D0BEC427 CRC64;

Query Match 82.3%; Score 79; DB 1; Length 406;
Best Local Similarity 83.3%; Pred. No. 5.6e-05;
Matches 15; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 VIFNYKGNVLINKDIRC 18
|||:||||| ||:|||||
DB 146 VIFSYKGNHLISKDIRC 163

RESULT 8
CRTC_SCHMA
ID CRTC_SCHMA STANDARD; PRT; 393 AA.
AC Q06814; Q26562;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE CALRETICULIN PRECURSOR (SM4 PROTEIN).
OS Schistosoma mansoni (Blood fluke).
OC Eukaryota; Metazoa; Platyhelminthes; Turbellarian Platyhelminths;
OC Rhabdiorhiza; Eulcithophora; Revertospermatia; Digenea; Strigeidida; Schistosomatoidea;
OC Neodermata; Trematoda; Digenea; Strigeidida; Schistosoma.
OX NCBI_TaxID-6183;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-PUERTO RICAN;
RX MEDLINE-93165070; PubMed-8433712;
RA Khalife J., Trottein F., Schacht A.-M., Godin C., Pierce R.J.,
RA Capron A.;
RT "Cloning of the gene encoding a Schistosoma mansoni antigen
RT homologous to human Ro/SS-A autoantigen";
RL Mol. Biochem. Parasitol. 57:193-202(1993).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-PUERTO RICAN;
RX MEDLINE-94187805; PubMed-8139623;
RA Khalife J., Pierce R.J., Godin C., Capron A.;
RT "Cloning and sequencing of the gene encoding Schistosoma mansoni
RT calreticulin";
RL Mol. Biochem. Parasitol. 62:313-315(1993).
CC -!- FUNCTION: THIS PROTEIN BINDS CALCIUM. THERE ARE BOTH HIGH AND
CC -!- AFFINITY CALCIUM-BINDING SITES.
CC -!- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM LUMEN.

CC -!- SIMILARITY: BELONGS TO THE CALRETICULIN FAMILY.
CC -----
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CC -----
DR EMBL: M93097; AAA29854.1; -;
DR EMBL: L24159; AAA19024.1; -;
DR HSP: P00268; 4RXN.
DR InterPro: IPR001580; Calreticulin.
DR Pfam: PF00262; ER-target.
DR PRINTS: PR00626; CALRETICULIN.
DR PROSITE: PS00803; Calreticulin; 1.
DR PROSITE: PS00804; CALRETICULIN_2; 1.
DR PROSITE: PS00805; CALRETICULIN_REPEAT; 1.
KW Endoplasmic reticulum; Calcium-binding; Repeat; Signal; Glycoprotein.
FT SIGNAL 1 16 POTENTIAL.
FT CHAIN 17 393 CALRETICULIN.
FT DOMAIN 189 254 4 X 12 AA APPROXIMATE REPEATS.
FT REPEAT 189 200 1-1.
FT REPEAT 209 220 1-2.
FT REPEAT 225 236 1-3.
FT REPEAT 243 254 1-4.
FT DOMAIN 257 295 3 X 11 AA APPROXIMATE REPEATS.
FT REPEAT 257 267 2-1.
FT REPEAT 271 281 2-2.
FT REPEAT 285 295 2-3.
FT CARBOHYD 27 27 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT DISULFID 135 161 BY SIMILARITY.
FT SITE 390 393 PREVENT SECRETION FROM ER.
FT CONFLICT 89 90 MV -> IL (IN REF. 2).
FT CONFLICT 188 207 MISSING (IN REF. 2).
FT CONFLICT 378 378 Y -> D (IN REF. 2).
SQ SEQUENCE 393 AA; 45397 MW; 45F59857C21940D2 CRC64;

Query Match 75.0%; Score 72; DB 1; Length 393;
Best Local Similarity 77.8%; Pred. No. 0.00065;
Matches 14; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 VIFNYKGNVINKDIRC 18
|||:|||||:|:|:|
DB 144 VIFNYKGNHLIKKEIPC 161

RESULT 9
RALL_ONCVO STANDARD; PRT; 388 AA.
AC P11012;
DT 01-JUL-1989 (Rel. 11, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE RAL-1 PROTEIN PRECURSOR (41 KDA LARVAL ANTIGEN).
GN RALI.
OS Onchocerca volvulus.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea;
OX Onchocercidae; Onchocerca.
OX NCBI_TaxID=6282;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94341871; PubMed=7520419;
RA Rokeach L.A., Zimmerman P.A., Unnasch T.R.;
RT "Epitopes of the Onchocerca volvulus RALI antigen, a member of the
RT calreticulin family of proteins, recognized by sera from patients
RT with onchocerciasis."
RL Infect. Immun. 62:3696-3704(1994).

RN SEQUENCE OF 53-388 FROM N.A.
RX MEDLINE=88273584; PubMed=2455736;
RA Unnasch T.R., Gallin M.Y., Soboslay P.T., Erttmann K.D., Greene B.M.;
RT "Isolation and characterization of expression cDNA clones encoding
RT antigens of Onchocerca volvulus infective larvae."
RL J. Clin. Invest. 82:262-269(1988).
CC -!- SIMILARITY: BELONGS TO THE CALRETICULIN FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: M20565; AAA59056.1; -;
DR PIR: A32507; A32507. Calreticulin.
DR InterPro: IPR001580; Calreticulin.
DR Pfam: PF00262; calreticulin; 1.
DR PRINTS: PR00626; CALRETICULIN.
DR PRODOM: PD001866; Calreticulin; 1.
DR PROSITE: PS00803; Calreticulin; 1.
DR PROSITE: PS00804; CALRETICULIN_2; 1.
DR PROSITE: PS00805; CALRETICULIN_REPEAT; 3.
KW Calcium-binding; Repeat; Antigen; Signal.
FT SIGNAL 1 17 POTENTIAL.
FT CHAIN 18 388 RAL-1 PROTEIN.
FT DOMAIN 189 253 4 X APPROXIMATE REPEATS.
FT REPEAT 189 200 1-1.
FT REPEAT 208 219 1-2.
FT REPEAT 225 236 1-3.
FT REPEAT 242 253 1-4.
FT DOMAIN 257 295 3 X APPROXIMATE REPEATS.
FT REPEAT 257 267 2-1.
FT REPEAT 271 281 2-2.
FT REPEAT 285 295 2-3.
FT DOMAIN 353 388 ARG/LYS-RICH (BASIC).
FT DISULFID 135 161 BY SIMILARITY.
SQ SEQUENCE 388 AA; 45298 MW; 9537F298A2D31CD6 CRC64;

Query Match 68.8%; Score 66; DB 1; Length 388;
Best Local Similarity 66.7%; Pred. No. 0.0054;
Matches 12; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 VIFNYKGNVINKDIRC 18
|||:|||||:|:|:|
DB 144 VIFHYKDRNHNMTKKDIRC 161

RESULT 10
CRTC_CAEEL
ID CRTC_CAEEL STANDARD; PRT; 395 AA.
AC P27798;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 01-FEB-1994 (Rel. 28, Last annotation update)
DE CALRETICULIN PRECURSOR.
GN CRT-1.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OX Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2;
RX MEDLINE=92329978; PubMed=1627827;
RA Smith M.J.;
RT "A C. elegans gene encodes a protein homologous to mammalian
RT calreticulin."
RL DNA Seq. 2:235-240(1992).

```
CC CC -!- FUNCTION: THIS PROTEIN BINDS CALCIUM. THERE ARE BOTH HIGH AND
CC CC LOW AFFINITY CALCIUM-BINDING SITES.
CC CC -!- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM LUMEN.
CC CC -!- SIMILARITY: BELONGS TO THE CALRETICULIN FAMILY.
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CC CC -----
CC CC EMBL; X59589; CAA42159.1; -
CC CC InterPro; IPR001580; Calreticulin.
CC CC Pfam; PF00262; calreticulin; 1.
CC CC PRINTS; PR00626; CALRETICULIN.
CC CC ProDom; PD001866; Calreticulin; 1.
CC CC PROSITE; PS00014; ER_TARGET; 1.
CC CC PROSITE; PS00803; CALRETICULIN_1; 1.
CC CC PROSITE; PS00804; CALRETICULIN_2; 1.
CC CC PROSITE; PS00805; CALRETICULIN_REPEAT; 3.
CC CC KW Endoplasmic reticulum; Calcium-binding; Repeat; Signal.
CC CC FT SIGNAL 1 2 POTENTIAL.
CC CC FT CHAIN 7 395 CALRETICULIN.
CC CC FT DOMAIN 7 192 N-DOMAIN.
CC CC FT DOMAIN 193 301 P-DOMAIN.
CC CC FT DOMAIN 302 395 C-DOMAIN.
CC CC FT DOMAIN 186 250 4 X APPROXIMATE REPEATS.
CC CC FT REPEAT 186 197 1-1.
CC CC FT REPEAT 205 216 1-2.
CC CC FT REPEAT 222 233 1-3.
CC CC FT REPEAT 239 250 1-4.
CC CC FT DOMAIN 254 292 3 X APPROXIMATE REPEATS.
CC CC FT REPEAT 254 264 2-1.
CC CC FT REPEAT 268 278 2-2.
CC CC FT REPEAT 282 292 2-3.
CC CC FT DOMAIN 332 390 ASP/GLU/LYS-RICH.
CC CC FT DISULFID 133 158 BY SIMILARITY.
CC CC FT SITE 392 395 PREVENT SECRETION FROM ER.
CC CC SEQUENCE 395 AA; 45616 MW; 35CA7D2EC1D56B03 CRC64;

Query Match 66.7%; Score 64; DB 1; Length 395;
Best Local Similarity 66.7%; Pred. No. 0.011;
Matches 12; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 VIFNYKGNVLINKDIRC 18
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DB 141 VILNYKGNKLINKEITC 158

RESULT 11
CRTC_CHLRE
ID CRTC_CHLRE STANDARD; PRT; 420 AA.
AC Q9STD3;
DT 20-AUG-2001 (Rel. 40, Created)
DT 20-AUG-2001 (Rel. 40, Last sequence update)
DE CALRTICULIN PRECURSOR.
OS Chlamydomonas reinhardtii.
OC Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
CX Chlamydomonadaceae; Chlamydomonas.
OX NCBI_TaxID 3055;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN 137C;
RA Zuppin A.; Kuydanov C.;
RT "cloning and characterization of a cDNA encoding Chlamydomonas
RT reinhardtii calreticulin.";
RL Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.
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CC CC -!- FUNCTION: THIS PROTEIN BINDS CALCIUM. THERE ARE BOTH HIGH AND
CC CC LOW AFFINITY CALCIUM-BINDING SITES (BY SIMILARITY).
CC CC -!- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM LUMEN (BY SIMILARITY).
CC CC -!- SIMILARITY: BELONGS TO THE CALRETICULIN FAMILY.
CC CC -----
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CC CC -----
CC CC EMBL; AJ000765; CAB54526.1; -
CC CC InterPro; IPR001580; Calreticulin.
CC CC Pfam; PF00262; calreticulin; 1.
CC CC PRINTS; PR00626; CALRETICULIN.
CC CC ProDom; PD001866; Calreticulin; 1.
CC CC PROSITE; PS00014; ER_TARGET; 1.
CC CC PROSITE; PS00803; CALRETICULIN_1; 1.
CC CC PROSITE; PS00804; CALRETICULIN_2; 1.
CC CC PROSITE; PS00805; CALRETICULIN_REPEAT; 1.
CC CC KW Endoplasmic reticulum; Calcium-binding; Repeat; Signal.
CC CC FT SIGNAL 1 18 POTENTIAL.
CC CC FT CHAIN 19 420 CALRETICULIN.
CC CC FT SITE 417 420 PREVENT SECRETION FROM ER (POTENTIAL).
CC CC SEQUENCE 420 AA; 47327 MW; DD3BAJAFBF61C9B CRC64;

Query Match 63.5%; Score 61; DB 1; Length 420;
Best Local Similarity 70.6%; Pred. No. 0.034;
Matches 12; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 VIFNYKGNVLINKDIR 17
  || ||||| || |||
DB 149 VILTYKGNLYLKDKIK 165

RESULT 12
CRTC_DICDI
ID CRTC_DICDI STANDARD; PRT; 424 AA.
AC Q23858;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DE CALRETICULIN PRECURSOR.
OS Dictyostelium discoideum (Slime mold).
OC Eukaryota; Mycetozoa; Dictyostelida; Dictyostelium.
OX NCBI_TaxID 44689;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-AX3;
RA Mueller-Taubenberger A.; Gerisch G.;
RL Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.
CC CC -!- FUNCTION: THIS PROTEIN BINDS CALCIUM. THERE ARE BOTH HIGH AND
CC CC LOW AFFINITY CALCIUM-BINDING SITES (BY SIMILARITY).
CC CC -!- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM LUMEN.
CC CC -!- SIMILARITY: BELONGS TO THE CALRETICULIN FAMILY.
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CC CC -----
CC CC EMBL; U36937; AAB87719.1; -
CC CC DictyDb; DD00042; -
CC CC InterPro; IPR001580; Calreticulin.
CC CC Pfam; PF00262; calreticulin; 1.
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DR PRINTS; PR00626; CALRETICULIN.
 DR PRODM; PD001866; Calreticulin; 1.
 DR PROSITE; PS00804; CALRETICULIN.2; 1.
 DR PROSITE; PS00805; CALRETICULIN_REPEAT; 1.
 DR PROSITE; PS00014; ER_TARGET; 1.
 KW Endoplasmic reticulum; Calcium-binding; Repeat; Signal.
 FT SIGNAL 1 19 POTENTIAL.
 FT CHAIN 20 424 CALRETICULIN.
 FT DOMAIN 191 257 4 X 12 AA APPROXIMATE REPEATS.
 FT REPEAT 191 202 1-1.
 FT REPEAT 211 222 1-2.
 FT REPEAT 227 238 1-3.
 FT REPEAT 246 257 1-4.
 FT REPEAT 260 298 3 X 11 AA APPROXIMATE REPEATS.
 FT REPEAT 260 270 2-1.
 FT REPEAT 274 284 2-2.
 FT REPEAT 288 298 2-3.
 FT DISULFID 105 137 BY SIMILARITY.
 FT SITE 421 424 PREVENT SECRETION FROM ER (POTENTIAL).
 SQ SEQUENCE 424 AA; 48350 MW; BAF273694FB6FC37 CRC64;

Query Match 61.5%; Score 59; DB 1; Length 424;
 Best Local Similarity 75.0%; Pred. No. 0.07;
 Matches 12; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 1 VIFNYKGNVINKDI 16
 || ||||| || ||
 Db 145 VILNYKGNHLKKEI 160

RESULT 13
 CRTX_EUGR STANDARD; PRT; 401 AA.
 AC Q92NY3;
 DT 20-AUG-2001 (Rel. 40, Created)
 DT 20-AUG-2001 (Rel. 40, Last sequence update)
 DT 20-AUG-2001 (Rel. 40, Last annotation update)
 DE CALRETICULIN PRECURSOR.
 OS Euglena gracilis.
 OC Eukaryota; Euglenozoa; Euglenida; Euglenales; Euglena.
 OX NCBI_TaxID=3039;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Navazzo L., Baldan B., Martin W., Mariani P.;
 RT "Evidence for conservation of a calcium homeostat component:
 purification characterization and cloning of calreticulin from Euglena
 gracilis.";
 RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: THIS PROTEIN BINDS CALCIUM. THERE ARE BOTH HIGH AND
 CC LOW AFFINITY CALCIUM-BINDING SITES (BY SIMILARITY).
 CC -!- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM LUMEN (BY SIMILARITY).
 CC -!- SIMILARITY: BELONGS TO THE CALRETICULIN FAMILY.
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 CC
 CC EMBL; AJ002057; CAA05161.1; -
 CC Mendel; 32549; Betvu; I166; 32549.
 DR InterPro; IPR001580; Calreticulin.
 DR InterPro; IPR000886; ER_target.
 DR Pfam; PF00262; calreticulin; 1.
 DR PRINTS; PR00626; CALRETICULIN.
 DR ProDom; PD001866; Calreticulin; 1.
 DR PROSITE; PS00014; ER_TARGET; 1.
 DR PROSITE; PS00803; CALRETICULIN.1; 1.
 DR PROSITE; PS00804; CALRETICULIN.2; 1.
 DR PROSITE; PS00805; CALRETICULIN_REPEAT; 2.
 KW Endoplasmic reticulum; Calcium-binding; Repeat; Signal; Glycoprotein.
 FT SIGNAL 1 25 POTENTIAL.
 FT CHAIN 26 416 CALRETICULIN.
 FT CARBOHYD 57 57 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 157 157 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT SITE 413 416 PREVENT SECRETION FROM ER (POTENTIAL).
 SQ SEQUENCE 416 AA; 48136 MW; 565FEC3489F77CA7 CRC64;

Query Match 55.2%; Score 53; DB 1; Length 416;
 Best Local Similarity 58.8%; Pred. No. 0.58;
 Matches 10; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

OY 2 IFNYKGNVINKDIRC 18
 ||||| || || ||
 Db 143 ILTYKGNLLWKKEPC 159

RESULT 14
 CRTX_BETVU STANDARD; PRT; 416 AA.
 AC O81919;
 DT 20-AUG-2001 (Rel. 40, Created)
 DT 20-AUG-2001 (Rel. 40, Last sequence update)
 DT 20-AUG-2001 (Rel. 40, Last annotation update)
 DE CALRETICULIN PRECURSOR.
 OS Beta vulgaris (Sugar beet).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Caryophyllales; Caryophyllaceae; Beta.
 OX NCBI_TaxID=3555;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=VV-D/ZR5; TISSUE=Leaf;
 RA Viereck R.;
 RT "Nucleotide sequence from sugar beet calreticulin.";
 RL Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: THIS PROTEIN BINDS CALCIUM. THERE ARE BOTH HIGH AND
 CC LOW AFFINITY CALCIUM-BINDING SITES (BY SIMILARITY).
 CC -!- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM LUMEN (BY SIMILARITY).
 CC -!- SIMILARITY: BELONGS TO THE CALRETICULIN FAMILY.
 CC
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 CC
 CC EMBL; AJ002057; CAA05161.1; -
 CC Mendel; 32549; Betvu; I166; 32549.
 DR InterPro; IPR001580; Calreticulin.
 DR InterPro; IPR000886; ER_target.
 DR Pfam; PF00262; calreticulin; 1.
 DR PRINTS; PR00626; CALRETICULIN.
 DR ProDom; PD001866; Calreticulin; 1.
 DR PROSITE; PS00014; ER_TARGET; 1.
 DR PROSITE; PS00803; CALRETICULIN.1; 1.
 DR PROSITE; PS00804; CALRETICULIN.2; 1.
 DR PROSITE; PS00805; CALRETICULIN_REPEAT; 2.
 KW Endoplasmic reticulum; Calcium-binding; Repeat; Signal; Glycoprotein.
 FT SIGNAL 1 25 POTENTIAL.
 FT CHAIN 26 416 CALRETICULIN.
 FT CARBOHYD 57 57 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 157 157 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT SITE 413 416 PREVENT SECRETION FROM ER (POTENTIAL).
 SQ SEQUENCE 416 AA; 48136 MW; 565FEC3489F77CA7 CRC64;

Query Match 55.2%; Score 53; DB 1; Length 416;
 Best Local Similarity 58.8%; Pred. No. 0.58;
 Matches 10; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

OY 2 IFNYKGNVINKDIRC 18
 ||||| || || ||
 Db 143 ILTYKGNLLWKKEPC 159

Db 153 IFNYNDTNHLIKKDVPC 169

RESULT 15

CRT3_ARATH

ID CRT3_ARATH STANDARD; PRT; 424 AA.

AC 004153; Q98JE7;

DT 20-AUG-2001 (Rel. 40, Created)

DT 20-AUG-2001 (Rel. 40, Last sequence update)

DT 20-AUG-2001 (Rel. 40, Last annotation update)

DE CALRETICULIN 3 PRECURSOR.

GN CRT3 OR T27G7.13.

OS Arabidopsis thaliana (Mouse-ear cress).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;

OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.

OX NCBI_TaxID:3702;

[1]

RN SEQUENCE FROM N.A.

RP MEDLINE 97303616; PubMed-9159940;

RA Nelson D.E., Glaunsinger B., Bohnert H.J.;

RT *Abundant accumulation of the calcium-binding molecular chaperone

RT calreticulin in specific floral tissues of Arabidopsis thaliana.*;

RL Plant Physiol. 114:29-37(1997).

[2]

RN SEQUENCE FROM N.A.

RP Shinn P., Brooks S., Buehler E., Chao Q., Johnson-Hopson C., Khan S.,

RA Kim C., Altafi H., Bel Q., Chin C., Chiou J., Chol E., Conn L.,

RA Conway A., Gonzales A., Hansen N., Howing B., Koo T., Lam B., Lee J.,

RA Lenz C., Li J., Liu A., Liu K., Liu S., Mukharasy N., Nguyen M.,

RA Palm C., Pham P., Sakano H., Schwartz J., Southwick A., Thaveri A.,

RA Toriumi M., Vaysberg M., Yu G., Federspiel N.A., Theologis A.,

RA Ecker J.R.;

RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.

CC -!- FUNCTION: THIS PROTEIN BINDS CALCIUM. THERE ARE BOTH HIGH AND

CC -!- LOW AFFINITY CALCIUM-BINDING SITES (BY SIMILARITY).

CC -!- SURCELLULAR LOCATION: ENDOPLASMIC RETICULUM LUMEN (BY SIMILARITY).

CC -!- SIMILARITY: BELONGS TO THE CALRETICULIN FAMILY.

CC -----

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CC or send an email to license@isb-sib.ch).

CC -----

DR EMBL; U66345; AAC49697.1; -.

DR EMBL; AC006932; AAF22902.1; ALT_SEQ.

DR Mende; 16507; Arath;1166;16507.

DR InterPro; IPR001580; Calreticulin.

DR InterPro; IPR000886; ER_target.

DR Pfam; PF00262; calreticulin; 1.

DR PRINTS; PR00626; CALRETICULIN.

DR PRODOM; PD001866; Calreticulin; 1.

DR PROSITE; PS00014; ER_TARGET; 1.

DR PROSITE; PS00803; CALRETICULIN_1; 1.

DR PROSITE; PS00804; CALRETICULIN_2; 1.

DR PROSITE; PS00805; CALRETICULIN_REPEAT; FALSE_NEG.

DR Endoplasmic reticulum; Calcium-binding; Repeat; Signal; Glycoprotein;

KW Multigene family.

FT SIGNAL 1 28 POTENTIAL.

FT CHAIN 29 424 CALRETICULIN 3

FT CARBOHYD 97 97 N-LINKED (GLCNAC. .) (POTENTIAL).

FT SITE 421 424 PREVENT SECRETION FROM ER (POTENTIAL).

FT CONFLICT 279 279 F -> S (IN REF. 2).

SQ SEQUENCE 424 AA; 49904 MW; 650E0AE8342F0B97 CRC64;

Query Match 54.2%; Score 52; DB 1; Length 424;

Best Local Similarity 50.0%; Pred. No. 0.84; Indels 0; Gaps 0;

Mutchnw 9; Conservative 5; Mismatches 4;

QY 1 VIFNYKGNVLINKDIRC 18

DB 155 VIVSYGQNYPIKKDLQC 172

Search completed: January 9, 2002, 15:12:15

Job time: 657 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: January 9, 2002, 15:02:03 ; Search time 43.73 Seconds
(without alignments)
31.355 Million cell updates/sec

Title: US-09-828-000-6

Perfect score: 96
Sequence: 1 VIFNYGKNVLINKDIRC 18

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_68:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	96	100.0	400	2 S43376	calreticulin, brai
2	96	100.0	416	1 S06763	calreticulin, precu
3	96	100.0	416	2 JH0819	calreticulin, precu
4	96	100.0	417	1 A37047	calreticulin, precu
5	96	100.0	418	1 A34154	calreticulin, precu
6	96	100.0	421	2 S36799	calreticulin, precu
7	86	89.6	405	1 JH0795	calreticulin, precu
8	79	82.3	406	2 A56637	calreticulin, homol
9	78	81.2	419	2 S71343	calreticulin, precu
10	73	76.0	384	2 S29130	calreticulin (clon
11	73	76.0	411	2 S29129	calreticulin, precu
12	72	75.0	393	1 A48573	calreticulin, autoa
13	66	68.8	336	2 A32507	41K larval antigen
14	64	66.7	395	2 S25851	calreticulin, precu
15	53	55.2	416	2 T14554	calreticulin - bee
16	51	53.1	725	1 IJMSNG	neural cell adhesi
17	51	53.1	761	1 IJHUNG	neural cell adhesi
18	51	53.1	853	1 IJBNOC	neural cell adhesi
19	51	53.1	858	1 IJRTNC	neural cell adhesi
20	51	53.1	1091	1 IJCHNL	neural cell adhesi
21	51	53.1	1115	1 IJMSNL	neural cell adhesi
22	48	50.0	464	2 A53101	vitamin D3 hydroxy
23	47	49.0	725	2 JE0099	neural cell adhesi
24	47	49.0	725	2 JE0100	neural cell adhesi
25	47	49.0	1088	1 IJXLNL	neural cell adhesi
26	47	49.0	1092	1 JN0635	neural cell adhesi
27	45	46.9	412	2 T05703	calreticulin - bar
28	45	46.9	415	2 T05705	calreticulin - bar
29	45	46.9	501	2 T44939	glyceraldehyde-3-p

30	44	45.8	417	2 A64380	phosphoglycerate k
31	44	45.8	421	2 S58170	calreticulin, precu
32	44	45.8	425	2 C96605	calreticulin (CrtI
33	44	45.8	496	2 S33597	protein kinase chk
34	43	44.8	103	2 G71141	hypothetical prote
35	43	44.8	247	2 PC4260	activin type I rec
36	43	44.8	257	2 C75077	iron (iii) abc tra
37	43	44.8	327	2 B82918	DNA-directed RNA p
38	43	44.8	415	2 T10172	calreticulin - cas
39	43	44.8	435	2 S23580	probable protein k
40	43	44.8	767	2 B84594	probable LRR recep
41	42	43.8	103	2 F75010	hypothetical prote
42	42	43.8	121	2 B56272	probable pheromone
43	42	43.8	154	2 A60998	replication protei
44	42	43.8	222	2 H71260	probable glucose-1
45	42	43.8	284	2 T49025	carbonate dehydrat

ALIGNMENTS

RESULT 1
S43376
calreticulin, brain isoform 1 - bovine
C:Species: Bos primigenius taurus (cattle)
C:Date: 20-Oct-1994 #sequence_revision 23-Mar-1995 #text_change 07-May-1999
C:Accession: S43376; S36801
R:Matsuoka, K.; Seta, K.; Yamakawa, Y.; Okuyama, T.; Shinoda, T.; Isobe, T.
Biochem. J. 298, 435-442, 1994
A:Title: Covalent structure of bovine brain calreticulin.
A:Reference number: S43376; MUID:94183174
A:Accession: S43376
A:Molecule type: protein
A:Residues: 1-400 <MAT>
A:Experimental source: brain
R:Liu, N.; Fine, R.E.; Johnson, R.J.
Biochim. Biophys. Acta 1202, 70-76, 1993
A:Title: Comparison of cDNAs from bovine brain coding for two isoforms of calreticuli
A:Reference number: S36799; MUID:93385184
A:Accession: S36801
A>Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 45-63, 'E', 65-83 <LIU>
A:Experimental source: brain, clone 8.1
C:Superfamily: calreticulin
C:Keywords: calcium binding; glycoprotein
F:397-400/Region: endoplasmic reticulum retention signal
F:120-146/Disulfide bonds: #status experimental
F:162/Binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match 100.0%; Score 96; DB 2; Length 400;
Best Local Similarity 100.0%; Pred. No. 1.5e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VIFNYGKNVLINKDIRC 18
|||||
Db 129 VIFNYGKNVLINKDIRC 146

RESULT 2
S06763
calreticulin precursor - mouse
N:Alternate names: 55K calcium-binding reticuloplasmin; calregulin
C:Species: Mus musculus (house mouse)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C:Accession: S06763; JG1444; PC1233; A57498
R:Smith, M.J.; Koch, G L.E.
EMBO J. 8, 3581-3586, 1989
A:Title: Multiple zones in the sequence of calreticulin (CRP55, calregulin, HACBP), a
A:Reference number: S06763; MUID:90059955
A:Accession: S06763
A:Molecule type: DNA

A:Residues: 1-416 <SMI>
A:Cross-references: EMBL:X14926; NID:g50567; PIDN:CAA33053.1; PID:g50568
R:Mazzarolla, R.A.; Gold, P.; Cunningham, M.; Green, M.
Gene 120, 217-225, 1992
A:Title: Determination of the sequence of an expressible cDNA clone encoding Erp60/calnexin
A:Reference number: JC1444; MUID:93013037
A:Accession: JC1444
A:Molecule type: mRNA
A:Residues: 1-416 <MAZ>
A:Cross-references: GB:M92988; NID:g193084; PIDN:AAA37569.1; PID:g193085
A:Accession: PC1233
A:Molecule type: protein
A:Residues: 18-41 <MAZ>
R:White, T.K.; Zhu, Q.; Tanzer, M.L.
J. Biol. Chem. 270, 15926-15929, 1995
A:Title: Cell surface calreticulin is a putative mannose lectin which triggers mouse m...
A:Reference number: A57498; MUID:95332280
A:Accession: A57498
A>Status: preliminary
A:Molecule type: protein
A:Residues: 74-80;142-151;186-193 <WHI>
C:Superfamily: calreticulin
C:Keywords: calcium binding
F:1-17/Domain: signal sequence #status predicted <SIG>
F:18-416/Product: calreticulin #status experimental <MAT>
F:413-416/Region: endoplasmic reticulum retention signal

Query Match 100.0%; Score 96; DB 1; Length 416;
Best Local Similarity 100.0%; Pred. No. 1.5e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VIFNYKGNVINKDIRC 18
|||||
DB 146 VIFNYKGNVINKDIRC 163

RESULT 3
JH0819
calreticulin precursor - rat
N:Alternate names: calcium-binding protein 3
C:Species: Rattus norvegicus (Norway rat)
C>Date: 30-Sep-1993 #sequence_revision 20-Aug-1994 #text_change 20-Jun-2000
C:Accession: JH0819; A91776; S11205; PC1109; S45036; S04867; S39372; A34473; S13045
R:Nakamura, M.; Moriya, M.; Baba, T.; Michikawa, Y.; Yamanobe, T.; Arai, K.; Okinaga, S.
Exp. Cell Res. 205, 101-110, 1993
A:Title: An endoplasmic reticulum protein, calreticulin, is transported into the acrosom...
A:Reference number: A49176; MUID:93202172
A:Accession: JH0819
A:Molecule type: mRNA
A:Residues: 1-416 <NAK>
A:Cross-references: GB:D78308; NID:g1089798; PIDN:BA11345.1; PID:g1845572
A:Accession: A49176
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-416 <NAZ>
A:Cross-references: GB:D78308; NID:g1089798; PIDN:BA11345.1; PID:g1845572
A:Experimental source: Sprague-Dawley, spermatogenic cells
A:Note: sequence extracted from NCBI backbone (NCBIN:127639, NCBIP:127643)
R:Murthy, K.K.; Banville, D.; Srikant, C.B.; Carrier, F.; Holmes, C.; Bell, A.; Patel, Y.
Nucleic Acids Res. 18, 4933, 1990
A:Title: Structural homology between the rat calreticulin gene product and the Onchocerc...
A:Reference number: S11205; MUID:90370496
A:Accession: S11205
A:Molecule type: mRNA
A:Residues: 1-416 <MUR>
A:Cross-references: EMBL:X53363; NID:g55854; PIDN:CAA37446.1; PID:g55855
R:Nakamura, M.; Michikawa, Y.; Baba, T.; Okinaga, S.; Arai, K.
Biochem. Biophys. Res. Commun. 186, 668-673, 1992
A:Title: Calreticulin is present in the acrosome of spermatids of rat testis.
A:Reference number: PC1109; MUID:92360010
A:Accession: PC1109
A:Molecule type: protein

A:Residues: 18-32 <NAK>
A:Experimental source: testis, strain Sprague-Dawley
R:Soenichsen, B.; Fuelekruug, J.; van Nguyen, P.; Diekmann, W.; Robinson, D.G.; Mies
submitted to the EMBL Data Library, May 1994
A:Description: Retention and retrieval: both mechanisms cooperate to maintain calretic...
A:Reference number: S45036
A:Accession: S45036
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-416 <SOE>
A:Cross-references: EMBL:X79327; NID:g488840; PIDN:CAA55890.1; PID:g488841
R:Lone, Y.C.; Bailly, A.; Latruffe, N.
submitted to the EMBL Data Library, December 1988
A:Reference number: S04867
A:Accession: S04867
A:Molecule type: mRNA
A:Residues: 'R', 270-358, 'AAG', <LON>
A:Cross-references: EMBL:X13702; NID:g56055; PIDN:CAA31987.1; PID:g930260
A:Note: the authors designated the protein as D-beta-hydroxybutyrate dehydrogenase
R:Yokoi, T.; Nagayama, S.; Kajiwara, R.; Kawaguchi, Y.; Horiuchi, R.; Kamataki, T.
Biochim. Biophys. Acta 1158, 339-344, 1993
A:Title: Identification of protein disulfide isomerase and calreticulin as autoimmune...
A:Reference number: S39371; MUID:94072621
A:Accession: S39372
A:Molecule type: protein
A:Residues: 18-23, 'X', 25-32 <VOK>
R:Van, P.N.; Peter, F.; Soelling, H.D.
J. Biol. Chem. 264, 17494-17501, 1989
A:Title: Four intracisternal calcium-binding glycoproteins from rat liver microsomes...
A:Reference number: A34473; MUID:90008920
A:Accession: A34473
A>Status: preliminary
A:Molecule type: protein
A:Residues: 18-36 <VAN>
R:Trevies, S.; de Mattei, M.; Lanfredi, M.; Villa, A.; Green, N.M.; MacLennan, D.H.; M...
Biochem. J. 271, 473-480, 1990
A:Title: Calreticulin is a candidate for a calsequestrin-like function in Ca(2+)-stor...
A:Reference number: S13045; MUID:91054414
A:Accession: S13045
A:Molecule type: protein
A:Residues: 18-29 <TRE>
C:Superfamily: calreticulin
C:Keywords: calcium binding; glycoprotein
F:1-17/Domain: signal sequence #status predicted <SIG>
F:18-416/Product: calreticulin #status experimental <MAT>
F:204-214/Region: nuclear location signal
F:413-416/Region: endoplasmic reticulum retention signal
F:344/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 100.0%; Score 96; DB 2; Length 416;
Best Local Similarity 100.0%; Pred. No. 1.5e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VIFNYKGNVINKDIRC 18
|||||
DB 146 VIFNYKGNVINKDIRC 163

RESULT 4
A37047
calreticulin precursor - human
N:Alternate names: 52K ribonucleoprotein autoantigen Ro/SS-A; 60K integrin-binding pr...
C:Species: Homo sapiens (man)
C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 18-Feb-2000
C:Accession: A42330; A37047; A46452; A28812; PH1525; A40346; S11475; T45075
R:McCaulliffe, D.P.; Yang, Y.S.; Wilson, J.; Sontheimer, R.D.; Capra, J.D.
J. Biol. Chem. 267, 2557-2562, 1992
A:Title: The 5'-flanking region of the human calreticulin gene shares homology with t...
A:Reference number: A42330; MUID:92129342
A:Accession: A42330
A:Molecule type: DNA

A:Residues: 1-417 <MC2>
A:Note: sequence extracted from NCBI backbone (NCBIN:78537, NCBIP:78536)
R:McCaulliffe, D.P.; Lux, F.A.; Lieu, T.S.; Sanz, I.; Hanke, J.; Newkirk, M.M.; Bachinski
J. Clin. Invest. 85, 1379-1391, 1990
A:Title: Molecular cloning, expression, and chromosome 19 localization of a human Ro/SS-
A:Reference number: A37047; MUID:90237213
A:Accession: A37047
A:Molecule type: mRNA
A:Residues: 1-417 <MC2>
A:Cross-references: GB:M32294; NID:g337486; PIDN:AAA36582.1; PID:g337487
A:Note: the authors translated the codon GTA for residue 349 as Tyr
R:Roekach, L.A.; Haselby, J.A.; Mellof, J.F.; Smeenk, R.J.; Unnasch, T.R.; Greene, B.M.;
J. Immunol. 147, 3031-3039, 1991
A:Title: Characterization of the autoantigen calreticulin.
A:Reference number: A46452; MUID:92013129
A:Accession: A46452
A:Molecule type: mRNA
A:Residues: 1-417 <ROK>
A:Cross-references: GB:M84739; NID:q179881; PIDN:AAA51916.1; PID:q179882
A:Note: sequence extracted from NCBI backbone (NCBIN:60749, NCBIP:60750)
R:Lieu, T.S.; Newkirk, M.M.; Capra, J.D.; Sontheimer, R.D.
J. Clin. Invest. 82, 96-101, 1988
A:Title: Molecular characterization of human Ro/SS-A antigen. Amino terminal sequence of
A:Reference number: A28812; MUID:88273610
A:Accession: A28812
A:Molecule type: protein
A:Residues: 18-41 <LIE>
A:Note: 18-Ala was also found
R:Dupuis, M.; Schaefer, E.; Krause, K.H.; Tschopp, J.
J. Exp. Med. 177, 1-7, 1993
A:Title: The calcium-binding protein calreticulin is a major constituent of lytic granul
A:Reference number: PH1525; MUID:93115648
A:Accession: PH1525
A:Molecule type: protein
A:Residues: 18-27 <DUP>
A:Experimental source: LAK cell
R:Nojima, M.V.; Finlay, B.B.; Gray, V.; Dedhar, S.
Biochemistry 30, 9859-9866, 1991
A:Title: In vitro interaction of a polypeptide homologous to human Ro/SS-A antigen (calr
A:Reference number: A40346; MUID:92002034
A:Accession: A40346
A:Molecule type: protein
A:Residues: 18-34, R' <ROU>
R:Krause, K.H.; Simmerman, H.K.B.; Jones, L.R.; Campbell, K.P.
Biochem. J. 270, 545-548, 1990
A:Title: Sequence similarity of calreticulin with a Ca(2+)-binding protein that co-purif
A:Reference number: S11475; MUID:90380058
A:Accession: S11475
A:Molecule type: protein
A:Residues: 18-32 <KRA>
R:Lamerdin, J.; McCreedy, P.; Stillwagen, S.; Ramirez, M.; Carrano, A.
submitted to the EMBL Data Library, November 1996
A:Description: Characterization by genomic sequence analysis of a gene-rich 111 kb regio
A:Reference number: Z22906
A:Accession: T45075
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-417 <LAM>
A:Cross-references: EMBL:AD000092; PIDN:AA511176.1
A:Experimental source: cell line 5H12-B; fibroblast
C:Comment: Autoantibodies specific for this protein are found in Sjogren's syndrome and
C:Genetics:
A:Gene: GDB:CALR
A:Cross-references: GDB:125179; OMIM:109091
A:Map position: 19p13.3-19p13.2
A:Introns: 31/1; 63/1; 133/1; 164/3; 234/3; 272/3; 320/3; 351/3
A:Note: CRTG
C:Superfamily: calreticulin
C:Keywords: calcium binding; integrin binding
F:1-17/Domain: signal sequence #status predicted <SIG>
F:18-417/Product: calreticulin #status predicted <MAT>
F:414-417/Region: endoplasmic reticulum retention signal

Query Match 100.0%; Score 96; DB 1; Length 417;
Best Local Similarity 100.0%; Pred. No. 1.5e-07;
Matches 18; Conservative 0; Mismatches 0; Gaps 0;

QY 1 VIFNYGKNVINKDIRC 18
|||||
DB 146 VIFNYGKNVINKDIRC 163

RESULT 5

A34154
calreticulin precursor, skeletal muscle - rabbit
C:Species: Oryctolagus cuniculus (domestic rabbit)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
A:Accession: A34154; S13047
R:Fliegel, L.; Burns, K.; MacLennan, D.H.; Reithmeier, R.A.F.; Michalak, M.
J. Biol. Chem. 264, 21522-21528, 1989
A:Title: Molecular cloning of the high affinity calcium-binding protein (calreticulin
A:Reference number: A34154; MUID:90094320
A:Accession: A34154
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-418 <FLI>
A:Cross-references: GB:J05138; NID:gl64858; PIDN:AAA31188.1; PID:gl64859
R:Treves, S.; de Mattei, M.; Lanfredi, M.; Villa, A.; Green, N.M.; MacLennan, D.H.; M
Biochem. J. 271, 473-480, 1990
A:Title: Calreticulin is a candidate for a calsequestrin-like function in Ca(2+)-stor
A:Reference number: S13045; MUID:91054414
A:Accession: S13047
A:Molecule type: protein
A:Residues: 19-32 <TRE>
C:Superfamily: calreticulin
C:Keywords: skeletal muscle
F:1-17/Domain: signal sequence #status predicted <SIG>
F:415-418/Region: endoplasmic reticulum retention signal

Query Match 100.0%; Score 96; DB 1; Length 418;
Best Local Similarity 100.0%; Pred. No. 1.5e-07;
Matches 18; Conservative 0; Mismatches 0; Gaps 0;

QY 1 VIFNYGKNVINKDIRC 18
|||||
DB 146 VIFNYGKNVINKDIRC 163

RESULT 6

S36799
calreticulin precursor, brain isoform 2 - bovine
C:Species: Bos primigenius taurus (cattle)
C:Date: 10-Dec-1993 #sequence_revision 23-Mar-1995 #text_change 13-Aug-1999
A:Accession: S36799; S36800
R:Liu, N.; Fine, R.E.; Johnson, R.J.
Biochim. Biophys. Acta 1202, 70-76, 1993
A:Title: Comparison of cDNAs from bovine brain coding for two isoforms of calreticuli
A:Reference number: S36799; MUID:93385184
A:Accession: S36799
A:Molecule type: mRNA
A:Residues: 1-421 <LIU>
A:Cross-references: GB:LI13462; NID:g348693; PIDN:AAC37307.1; PID:g348694
A:Experimental source: brain, clone 9.4
A:Accession: S36800
A:Molecule type: protein
A:Residues: 35-45 <LI2>
C:Superfamily: calreticulin
C:Keywords: calcium binding; glycoprotein
F:1-34/Domain: signal sequence #status predicted <SIG>
F:35-421/Product: calreticulin, brain isoform 2 #status predicted <MAT>
F:418-421/Region: endoplasmic reticulum retention signal
F:141-167/Disulfide bonds: #status predicted
F:183/Binding site: carbohydrate (Asn) (covalent) #status predicted

A:Cross-references: EMBL:X67598

A:Accession: T01068

A:Status: translated from GB/EMBL/DBDJ

A:Molecule type: mRNA

A:Residues: 1-339, 'XTGR' <TRW>

A:Cross-references: EMBL:X67598; NID:g64610; PIDN:CAA47867.1; PID:g64611

A:Experimental source: CNS

C:Superfamily: calreticulin

C:Keywords: glycoprotein

F:381-384/Region: endoplasmic reticulum retention signal

F:316/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match

Best Local Similarity 76.0%; Score 73; DB 2; Length 384;

Matches 14; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 VIFNYKGNVLINKDIRC 18

||||| ||| ||| ||| |||

DB 118 VIFQYKKRNQLINKDIRC 135

RESULT 11

S29129

calreticulin precursor (clone 3) - African clawed frog (fragment)

C:Species: Xenopus laevis (African clawed frog)

C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 13-Aug-1999

A:Accession: S29129

R:Trevise, S.; Zorzato, F.; Pozzan, T.

Biochem. J. 287, 579-581, 1992

A:Title: Identification of calreticulin isoforms in the central nervous system.

A:Reference number: S29129; MUID:93074997

A:Accession: S29129

A:Molecule type: mRNA

A:Residues: 1-411 <TRE>

A:Cross-references: EMBL:X67597; NID:g64608; PIDN:CAA47866.1; PID:g64609

C:Superfamily: calreticulin

C:Keywords: glycoprotein

F:1-12/Domain: signal sequence (fragment) #status predicted <SIG>

F:13-411/Product: calreticulin #status predicted <MAT>

F:408-411/Region: endoplasmic reticulum retention signal

F:339/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match

Best Local Similarity 76.0%; Score 73; DB 2; Length 411;

Matches 14; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 VIFNYKGNVLINKDIRC 18

||||| ||| ||| ||| |||

DB 141 VIFQYKKRNQLINKDIRC 158

RESULT 12

A48573

calreticulin autoantigen homolog precursor - fluke (Schistosoma mansoni)

C:Species: Schistosoma mansoni

C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999

A:Accession: A48573

R:Khalife, J.; Trottein, F.; Schacht, A.M.; Godin, C.; Pierce, R.J.; Capron, A.

Mol. Biochem. Parasitol. 57, 193-202, 1993

A:Title: Cloning of the gene encoding a Schistosoma mansoni antigen homologous to human

A:Reference number: A48573; MUID:93165070

A:Accession: A48573

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-393 <KHA>

A:Cross-references: GB:M93097; NID:g160928

A:Note: sequence inconsistent with the nucleotide translation

C:Superfamily: calreticulin

F:1-16/Domain: signal sequence #status predicted <SIG>

F:390-393/Region: endoplasmic reticulum retention signal

Query Match

Best Local Similarity 75.0%; Score 72; DB 1; Length 393;

Matches 14; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 VIFNYKGNVLINKDIRC 18

||||| ||| ||| ||| |||

DB 144 VIFNYKGNHLIKKEIPC 161

RESULT 13

A32507

41k larval antigen - nematode (Onchocerca volvulus) (fragment)

C:Species: Onchocerca volvulus

C:Date: 21-May-1990 #sequence_revision 21-May-1990 #text_change 12-Apr-1995

C:Accession: A32507; A28813

R:Unnasch, T.R.; Gallin, M.Y.; Soboslay, P.T.; Erttmann, K.D.; Greene, B.M.

J. Clin. Invest. 82, 262-269, 1988

A:Title: Isolation and characterization of expression cDNA clones encoding antigens o

A:Reference number: A92769; MUID:88273584

A:Accession: A32507

A:Molecule type: mRNA

A:Residues: 1-336 <ONN>

C:Superfamily: calreticulin

Query Match

Best Local Similarity 68.8%; Score 66; DB 2; Length 336;

Matches 12; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 VIFNYKGNVLINKDIRC 18

||||| ||| ||| ||| |||

DB 92 VIFHYKDRNHMIKKDIRC 109

RESULT 14

S25851

calreticulin precursor - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C:Date: 06-Jan-1994 #sequence_revision 10-Nov-1995 #text_change 05-Nov-1999

C:Accession: S25851; T33996

R:Smith, M.J.

DNA Seq. 2, 235-240, 1992

A:Title: A C. elegans gene encodes a protein homologous to mammalian calreticulin.

A:Reference number: S25851; MUID:92329978

A:Accession: S25851

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-395 <SMI>

A:Cross-references: EMBL:X59589; NID:g6693; PIDN:CAA42159.1; PID:g6694

R:Bauer, C.; Courtney, L.; Laplant, Y.

submitted to the EMBL Data Library, February 1999

A:Description: The sequence of C. elegans cosmid Y38A10A.

A:Reference number: Z21453

A:Accession: T33996

A:Status: preliminary; translated from GB/EMBL/DBDJ

A:Molecule type: DNA

A:Residues: 1-395 <BAU>

A:Cross-references: EMBL:AF125963; PIDN:AAD14746.1; GSPDB:GN00023; CESP:Y38A10A.5

A:Experimental source: strain Bristol N2; clone Y38A10A

C:Genetics:

A:Gene: CESP:Y38A10A.5

A:Map position: 5

A:Introns: 107/3; 315/3

C:Superfamily: calreticulin

F:1-15/Domain: signal sequence #status predicted <SIG>

F:392-395/Region: endoplasmic reticulum retention signal

Query Match

Best Local Similarity 66.7%; Score 64; DB 2; Length 395;

Matches 12; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 VFNYGKNVINKDIRC 18
 || ||||: || ||: |
 Db 141 VILNYKGKLNKLNKEITC 158

RESULT 15

T14554
 calreticulin - beet
 C:Species: Beta vulgaris (beet)
 C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Jun-2000
 C:Accession: T14554
 K:Viereck, R.
 submitted to the EMBL Data Library, October 1997
 A:Description: Nucleotide sequence from sugar beet calreticulin.
 A:Reference number: Z18137
 A:Accession: T14554
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-416 <VIE>
 A:Cross-references: EMBL:AJ002057
 A:Experimental source: strain diploide Inzuchtlinie KWS; leaf
 C:Superfamily: calreticulin
 C:Keywords: calcium binding

Query Match 55.2%; Score 53; DB 2; Length 416;
 Beet Local Similarity 58.8%; Pred. No. 0.98;
 Matches 10; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 2 IFNYGKNVINKDIRC 18
 |||| | || ||: |
 Db 153 IFNYDTHLKKDVPC 169

Search completed: January 9, 2002, 15:02:03
 Job time: 190 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 9, 2002, 15:03:28 ; Search time 78.15 Seconds
(without alignments)
50.536 Million cell updates/sec

Title: US-09-828-000-5
Perfect score: 151
Sequence: 1 CGPGTKKVVHVIENYKGNVLINKDIRC 27

Scoring table:
BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 473505 seqs, 146272329 residues

Total number of hits satisfying chosen parameters: 473505

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_17:*
1: sp-archaea:*
2: sp-bacteria:*
3: sp-fungi:*
4: sp-human:*
5: sp-invertebrate:*
6: sp-mammal:*
7: sp-mhc:*
8: sp-organelle:*
9: sp-phage:*
10: sp-plant:*
11: sp-rodent:*
12: sp-virus:*
13: sp-vertebrate:*
14: sp-unclassified:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	144	95.4	318	13	Q9PTX7 lampetra re
2	142	94.0	421	5	Q9U6S0 strongyloce.
3	141	93.4	405	5	Q26268 aplysia cal
4	140	92.7	410	5	Q16893 amblyomma a
5	134	88.7	406	5	Q9U916 drosophila
6	128	84.8	375	5	Q18478 litomosoid
7	128	84.8	387	5	Q97372 dirofilaria
8	125	82.8	419	13	Q98984 rana rugosa
9	120	79.5	343	13	Q91711 xenopus lae
10	120	79.5	411	13	Q91710 xenopus lae
11	115	76.2	417	13	Q9PUC1 brachydanio
12	109.5	72.5	403	5	O76961 necator ame
13	108	71.5	350	5	Q26514 schistosoma
14	108	71.5	396	5	O45034 schistosoma
15	99	65.6	321	13	Q9U5G0 eptatretus
16	84	55.6	412	10	Q40040 hordeum vul
17	84	55.6	415	10	Q40041 hordeum vul
18	83	55.0	321	10	Q41799 zea mays (m
19	83	55.0	421	10	Q43712 zea mays (m

20	80.5	53.3	427	10	Q9FYV2	O9fyv2 pinus taeda
21	80	53.0	422	10	O22502	O22502 brassica na
22	76	50.3	240	10	Q9ST29	Q9st29 solanum mel
23	76	50.3	389	10	Q40567	Q40567 nicotiana t
24	61	40.4	70	10	Q9SXW3	Q9sxw3 lithospermu
25	57	37.7	137	11	Q9D373	Q9d373 mus musculus
26	57	37.7	380	11	Q9D9Q6	Q9d9q6 mus musculus
27	54	35.8	720	1	O73946	O73946 pyrococcus
28	53	35.1	764	2	Q9HXE0	Q9hxe0 pseudomonas
29	51	33.8	348	4	O00557	O00557 homo sapien
30	50.5	33.4	499	11	Q9DBB3	Q9dbb3 mus musculus
31	50	33.1	275	2	O9A131	O9a131 streptococc
32	50	33.1	304	3	O00867	O00867 nectria hae
33	50	33.1	708	5	Q9GVA7	Q9gva7 pimpla hypo
34	50	33.1	783	2	Q9LAW0	Q9law0 mycoplasma
35	49	32.5	434	12	O69017	O69017 ictalurid h
36	49	32.5	506	13	O73736	O73736 brachydanio
37	49	32.5	506	13	Q9DGI6	Q9dgi6 brachydanio
38	49	32.5	654	12	Q9DUB1	Q9dubl tt virus..o
39	48.5	32.1	89	2	P96636	P96636 bacillus su
40	48.5	32.1	1765	5	Q26791	Q26791 trypanosoma
41	48.5	32.1	1765	5	Q26794	Q26794 trypanosoma
42	48	31.8	183	1	O28949	O28949 archaeoglob
43	48	31.8	247	2	O48830	O48830 lactobacill
44	48	31.8	846	13	O57577	O57577 cynops pyrr
45	48	31.8	1100	13	O57576	O57576 cynops pyrr

ALIGNMENTS

RESULT 1

Q9PTX7 ID Q9PTX7 PRELIMINARY: PRT: 318 AA.
AC Q9PTX7:
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DE 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE CALRETICULIN (FRAGMENT).
OS Lampetra reissneri.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Hypercoartia;
OC Petromyzontiformes; Petromyzontidae; Lampetra.
OX NCBI_TaxID=7753;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20063780; PubMed=10594174;
RA Kuraku S., Hoshiyama D., Katoh K., Suga H., Miyata T.;
RT "Monophyly of lampreys and hagfishes supported by nuclear DNA-coded genes.";
RL J. Mol. Evol. 49:729-735(1999).
DR EMBL; AB025328; BAA88481.1; .
DR InterPro; IPR000886; ER.target.
DR InterPro; IPR001580; Calreticulin.
DR Pfam; PF00262; calreticulin; 1.
DR PRINTS; PR00626; CALRETICULIN.
DR PRODOM; PD001866; Calreticulin; 1.
DR PROSITE; PS00804; CALRETICULIN_2; 1.
DR PROSITE; PS00805; CALRETICULIN_REPEAT; 3.
DR PROSITE; PS00014; ER_TARGET; UNKNOWN_1.
FT NON_TER 1
SQ SEQUENCE 318 AA; 36997 MW; C88102EA1CAC1506 CRC64;

Query Match 95.4%; Score 144; DB 13; Length 318;

Best Local Similarity 96.3%; Pred No. 1.3e-12;

Matches 26; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CGPGTKKVVHVIENYKGNVLINKDIRC 27

Db 36 CGPGTKKVVHVIENYKGNVLINKDIRC 62

RESULT 2

Q906S0
ID Q906S0 PRELIMINARY; PRT; 421 AA.
AC Q906S0
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)
DE CALRETICULIN PRECURSOR.
GN CALRET.
OS Strongylocentrotus purpuratus (Purple sea urchin).
OC Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
OC Echinozoa; Echinoidae; Echinacea; Echinoida; Strongylocentrotidae;
OC Strongylocentrotus.
OX NCBI_TaxID 7668;
RN [1]
RP SEQUENCE FROM N.A.
RA Susan J.M., Just M.L., Lennarz W.J.;
RT "Cloning and Characterization of AlphaP Integrin and Calreticulin in
Embryos of the Sea Urchin."
RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
RL EMBL: AF177915; AAD55725.1; -.
DR InterPro: IPR000886; ER_target.
DR InterPro: IPR001580; Calreticulin.
DR Pfam: PF00262; calreticulin; 1.
DR PRINTS: PR00626; CALRETICULIN.
DR ProDom: PD001866; Calreticulin; 1.
DR PROSITE: PS00804; CALRETICULIN_2; 1.
DR PROSITE: PS00805; CALRETICULIN_REPEAT; 3.
DR PROSITE: PS00014; ER_TARGET; UNKNOWN_1.
KW Signal.
FT SIGNAL. 1 19 POTENTIAL.
FT CHAIN 20 421 CALRETICULIN.
SQ SEQUENCE 421 AA; 48822 MW; 172C664F59F41F93 CRC64;

Query Match 94.0%; Score 142; DB 5; Length 421;
Best Local Similarity 92.6%; Pred. No. 3.5e-12;
Matches 25; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 CGPGTKKVVHVIYKGNVLINKDIRC 27
Db 136 CGPGTKKVVHVIYKGNVLINKDIRC 162

RESULT 3
ID Q26268 PRELIMINARY; PRT; 405 AA.
AC Q26268
DT 01-NOV-1996 (Tremblrel. 01, Created)
DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)
DE CALRETICULIN
OS Aplysia californica (California sea hare).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Opisthobranchia; Anasplida;
OC Aplysiidae; Aplysia.
OX NCBI_TaxID: 6500;
RN [1]
RP SEQUENCE FROM N.A.
RA Kennedy T.E., Kuhl D., Barzilai A., Sweatt J.D., Kandel E.R.;
RT "Long-term sensitization training in Aplysia leads to an increase in
calreticulin, a major presynaptic calcium-binding protein.";
RL Neuron 9:1013-1024(1992).
DR EMBL: S51239; A824569.1; -.
DR InterPro: IPR000886; ER_target.
DR InterPro: IPR001580; Calreticulin.
DR Pfam: PF00262; calreticulin; 1.
DR PRINTS: PR00626; CALRETICULIN.
DR ProDom: PD001866; Calreticulin; 1.
DR PROSITE: PS00803; CALRETICULIN_1; 1.
DR PROSITE: PS00804; CALRETICULIN_2; 1.
DR PROSITE: PS00805; CALRETICULIN_REPEAT; 3.
DR PROSITE: PS00014; ER_TARGET; UNKNOWN_1.
SQ SEQUENCE 405 AA; 46738 MW; 14CAA201840DID69 CRC64;

Query Match 93.4%; Score 141; DB 5; Length 405;
Best Local Similarity 88.9%; Pred. No. 4.6e-12;
Matches 24; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 CGPGTKKVVHVIYKGNVLINKDIRC 27
Db 133 CGPGTKKVVHVIYKGNVLINKDIRC 159

RESULT 4
ID Q16893 PRELIMINARY; PRT; 410 AA.
AC Q16893
DT 01-NOV-1996 (Tremblrel. 01, Created)
DT 01-JAN-1999 (Tremblrel. 09, Last sequence update)
DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)
DE CALRETICULIN.
GN CRT-1.
OS Amblyomma americanum.
OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Acari;
OC Parasitiformes; Ixodida; Ixodidae; Amblyomma.
OX NCBI_TaxID 6943;
RN [1]
RP SEQUENCE OF 49-410 FROM N.A.
RC TISSUE-SALIVARY GLANDS;
RA Jaworski D.C., Simmen F.A., Lamoreaux W.J., Coons L.B., Muller M.T.,
RT Needham G.R.;
RT "A secreted calreticulin protein in Ixodid tick (Amblyomma americanum)
saliva";
RL J. Insect Physiol. 41:369-375(1995).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE-SALIVARY GLANDS;
RA Jaworski D.C.;
RL Submitted (MAR-1994) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE-SALIVARY GLANDS;
RA Fain-Thornton J.M., Jaworski D.C., Needham G.R.;
RL Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL: U07708; AAC79094.1; -.
DR InterPro: IPR000886; ER_target.
DR InterPro: IPR001580; Calreticulin.
DR Pfam: PF00262; calreticulin; 1.
DR PRINTS: PR00626; CALRETICULIN.
DR ProDom: PD001866; Calreticulin; 1.
DR PROSITE: PS00803; CALRETICULIN_1; 1.
DR PROSITE: PS00805; CALRETICULIN_REPEAT; 3.
DR PROSITE: PS00014; ER_TARGET; UNKNOWN_1.
SQ SEQUENCE 410 AA; 47485 MW; 32CCB8750A17DC54 CRC64;

Query Match 92.7%; Score 140; DB 5; Length 410;
Best Local Similarity 92.6%; Pred. No. 6.5e-12;
Matches 25; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 CGPGTKKVVHVIYKGNVLINKDIRC 27
Db 136 CGPGTKKVVHVIYKGNVLINKDIRC 162

RESULT 5
ID Q90916 PRELIMINARY; PRT; 406 AA.
AC Q90916
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)
DE CALRETICULIN.
GN CRC OR CG9429.
OS Drosophila melanogaster (Fruit fly).

OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=OREGON-R;
 RA Dodo K., Sakoyama Y., Gamo S.;
 RT "Drosophila melanogaster calreticulin for mRNA.";
 RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB00718; BAA85379.1; -;
 DR FlyBase; FBgn005585; Crc.
 DR InterPro; IPR001580; Calreticulin.
 DR InterPro; IPR000886; ER-target.
 DR Pfam; PF00262; calreticulin; 1.
 DR PRINTS; PR00626; CALRETICULIN.
 DR ProDom; PD001866; Calreticulin; 1.
 DR PROSITE; PS00803; CALRETICULIN_1; 1.
 DR PROSITE; PS00804; CALRETICULIN_2; 1.
 DR PROSITE; PS00805; CALRETICULIN_REPEAT; 3.
 DR PROSITE; PS00014; ER_TARGET; UNKNOWN_1.
 SQ SEQUENCE 406 AA; 46809 MW; 68BA49A6B81CC427 CRC64;

Query Match 88.7%; Score 134; DB 5; Length 406;
 Best Local Similarity 88.9%; Pred. No. 4.6e-11;
 Matches 24; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 CGPGTKKHVHIFNYKGNVINKDIRC 27
 |||||
 DB 137 CGPGTKKHVHIFNYKGNVINKDIRC 163

RESULT 6
 O18478 PRELIMINARY; PRT; 375 AA.

AC O18478; PRELIMINARY; PRT; 375 AA.
 DT 01-JAN-1998 (TrEMBLrel. 05, Created)
 DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
 DE RAL-1 PROTEIN (FRAGMENT).
 OS Litomosoides sigmodontis.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea;
 OC Onchocercidae; Litomosoides.
 OX NCBI_TaxID=42156;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MacLennan K., Hoffman W.H., Taylor D.W.;
 RL Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AJ001621; CAA04877.1; -;
 DR InterPro; IPR001580; Calreticulin.
 DR Pfam; PF00262; calreticulin; 1.
 DR PRINTS; PR00626; CALRETICULIN.
 DR ProDom; PD001866; Calreticulin; 1.
 DR PROSITE; PS00803; CALRETICULIN_1; 1.
 DR PROSITE; PS00804; CALRETICULIN_2; 1.
 DR PROSITE; PS00805; CALRETICULIN_REPEAT; 3.
 FT NON_TER 375
 SQ SEQUENCE 375 AA; 43842 MW; 03F7642FBFF7A5B8 CRC64;

Query Match 84.8%; Score 128; DB 5; Length 375;
 Best Local Similarity 81.5%; Pred. No. 3e-10;
 Matches 22; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 CGPGTKKHVHIFNYKGNVINKDIRC 27
 |||||
 DB 135 CGPGTKKHVHIFNYKGNVINKDIRC 161

RESULT 7
 O97372 PRELIMINARY; PRT; 387 AA.
 ID O97372

AC O97372;
 DT 01-MAY-1999 (TrEMBLrel. 10, Created).
 DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
 DE CALRETICULIN PRECURSOR.
 OS Dirofilaria immitis.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea;
 OC Onchocercidae; Dirofilaria.
 OX NCBI_TaxID=6287;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99094497; PubMed=9879888;
 RA Tsuji N., Morales T.H., Ozols V.V., Carmody A.B., Chandrashekar R.;
 RT "Molecular characterization of a calcium-binding protein from the
 RT filarial parasite Dirofilaria immitis.";
 RL Mol. Biochem. Parasitol. 97:69-79(1998).
 DR EMBL; AF052978; AAD03405.1; -;
 DR InterPro; IPR001580; Calreticulin.
 DR Pfam; PF00262; calreticulin; 1.
 DR PRINTS; PR00626; CALRETICULIN.
 DR ProDom; PD001866; Calreticulin; 1.
 DR PROSITE; PS00803; CALRETICULIN_1; 1.
 DR PROSITE; PS00804; CALRETICULIN_2; 1.
 DR PROSITE; PS00805; CALRETICULIN_REPEAT; 3.
 KW Signal.
 FT SIGNAL 1 18 POTENTIAL..
 FT CHAIN 19 387 CALRETICULIN.
 SQ SEQUENCE 387 AA; 44941 MW; E7741BF6AFA5885 CRC64;

Query Match 84.8%; Score 128; DB 5; Length 387;
 Best Local Similarity 81.5%; Pred. No. 3.1e-10;
 Matches 22; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 CGPGTKKHVHIFNYKGNVINKDIRC 27
 |||||
 DB 135 CGPGTKKHVHIFNYKGNVINKDIRC 161

RESULT 8
 O98984 PRELIMINARY; PRT; 419 AA.
 ID O98984
 AC O98984;
 DT 01-FEB-1997 (TrEMBLrel. 02, Created)
 DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
 DE CALRETICULIN.
 OS Rana rugosa (Frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Rana.
 OX NCBI_TaxID=8410;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96234004; PubMed=8654561;
 RA Yamamoto S., Nakamura M.;
 RT "Calnexin: its molecular cloning and expression in the liver of the
 RT frog, Rana rugosa.";
 RL FEBS Lett. 387:27-32(1996).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Yamamoto S.;
 RT "Strong expression of the calreticulin gene in the liver of Rana
 RT rugosa Tadpoles.";
 RL J. Exp. Zool. 0:0-0(1996).
 DR EMBL; D78589; BAA11425.1; -;
 DR InterPro; IPR000886; ER-target.
 DR InterPro; IPR001580; Calreticulin.
 DR Pfam; PF00262; calreticulin; 1.
 DR PRINTS; PR00626; CALRETICULIN.
 DR ProDom; PD001866; Calreticulin; 1.
 DR PROSITE; PS00803; CALRETICULIN_1; 1.
 DR PROSITE; PS00804; CALRETICULIN_2; 1.
 DR PROSITE; PS00805; CALRETICULIN_REPEAT; 3.


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ID O76961 PRELIMINARY; PRT; 403 AA.
AC Q76961;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE CALRETICULIN PRECURSOR.
GN CRT.
GE Necator americanus.
OS Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Strongylida;
OC Ancylostomatoidae; Ancylostomidae; Bunostominae; Necator.
NCBI_TaxID=51031;
RN [1]
RP SEQUENCE FROM N.A.
RA Pritchard D.I., Brown A., McElroy P., Loukas A., Girdwood K.,
RR Berry C., Fullkrug R., Beck E.;
RL "Calreticulin is a hookworm allergen.";
RT Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.
DR EMBL: AJ006790; CA007254.1; -
DE InterPro: IPR000886; ER_target.
DR InterPro: IPR001580; Calreticulin; 1.
DR Pfam: PF00262; calreticulin; 1.
DR PRINTS: PR00626; CALRETICULIN.
DR ProDom: PD001866; Calreticulin; 1.
DR PROSITE: PS00803; CALRETICULIN_1; 1.
DR PROSITE: PS00804; CALRETICULIN_2; 1.
DR PROSITE: PS00805; CALRETICULIN_REPEAT; 3.
DR PROSITE: PS00014; ER_TARGET; UNKNOWN_1.
KW Signal; Allergen.
FT SIGNAL 1 16 POTENTIAL.
SQ SEQUENCE 403 AA; 46833 MW; 21F38B0515487B6F CRC64;
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DR Pfam: PF00262; calreticulin; 1.
DR PRINTS: PR00626; CALRETICULIN.
DR ProDom: PD001866; Calreticulin; 1.
DR PROSITE: PS00804; CALRETICULIN_2; 1.
DR PROSITE: PS00805; CALRETICULIN_REPEAT; 3.
DR PROSITE: PS00014; ER_TARGET; UNKNOWN_1.
FT NON_TER 1
SQ SEQUENCE 321 AA; 37367 MW; 6E8DFA98D42F7AEF CRC64;

Query Match 65.6%; Score 99; DB 13; Length 321;
Best local similarity 66.7%; Pred. No. 3.3e-06;
Matches 18; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 1 CGPGTKKKVHVIFNYKGNVLINKDIRC 27
DB 36 CGYSTAKKVVHVLNSKGNHLIRKEVRC 62

Search completed: January 9, 2002, 15:03:28
Job time: 270 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: January 9, 2002, 15:12:15 ; Search time 25.18 Seconds
(without alignments)
39.315 Million cell updates/sec

Title: US-09-828-000-5

Perfect score: 151

Sequence: 1 CGPCTKKVHVIFNYKGNVLINKDIRC 27

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 100059 seqs, 36664827 residues

Total number of hits satisfying chosen parameters: 100059

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_39:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	151	100.0	400	1	CRT1_BOVIN
2	151	100.0	416	1	CRTC_MOUSE
3	151	100.0	416	1	CRTC_RAT
4	151	100.0	417	1	CRTC_HUMAN
5	151	100.0	418	1	CRTC_RABIT
6	151	100.0	421	1	CRT2_BOVIN
7	134	88.7	406	1	CRTC_DROME
8	121	80.1	388	1	RALL_ONCVO
9	112	74.2	393	1	CRTC_SCHMA
10	97	64.2	420	1	CRTC_CHLRE
11	96.5	63.9	395	1	CRTC_CAEEL
12	92	60.9	416	1	CRTC_BETVU
13	88	58.3	424	1	CRT3_ARATH
14	87	57.6	421	1	CRTC_PRUAR
15	87	57.6	424	1	CRTC_ARATH
16	83.5	55.3	424	1	CRTC_DICDI
17	83	55.0	424	1	CRTC_ORYSA
18	83	55.0	425	1	CRT1_ARATH
19	82.5	54.6	401	1	CRTC_EUGGR
20	82	54.3	415	1	CRTC_RICCO
21	76	50.3	416	1	CRTC_NICPL
22	71	47.0	420	1	CRTC_MAIZE
23	68	45.0	416	1	CRTC_BERST
24	53	35.1	463	1	VDAH_CHICK
25	52	34.4	1938	1	MYSD_CAEEL
26	51	33.8	560	1	YECO_YEAST
27	51	33.8	725	1	NCA2_MOUSE
28	51	33.8	761	1	NCA2_HUMAN
29	51	33.8	848	1	NCA1_HUMAN
30	51	33.8	853	1	NCA1_BOVIN
31	51	33.8	858	1	NCA1_RAT
32	51	33.8	1091	1	NCA1_CHICK
33	51	33.8	1115	1	NCA1_MOUSE

Query Match 100.0%; Score 151; DB 1; Length 400;
Best Local Similarity 100.0%; Pred. No. 2.4e-14;

ALIGNMENTS

RESULT 1

ID	CRT1_BOVIN	STANDARD;	PRT;	400 AA.
AC	P52193;			
DT	01-OCT-1996 (Rel. 34, Created)			
DT	01-OCT-1996 (Rel. 34, Last sequence update)			
DT	01-OCT-1996 (Rel. 34, Last annotation update)			
DE	CALRETICULIN, BRAIN ISOFORM 1 (CRP55) (CALREGULIN) (HACBP).			
OS	Bos taurus (Bovine).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;			
OC	Bovidae; Bovinae; Bos.			
OX	NCBI_TaxID=9913;			
RN	[1]			
RP	SEQUENCE.			
RC	TISSUE=Brain;			
RX	MEDLINE=941183174; PubMed=8135753;			
RA	Matsuoka K., Seta K., Yamakawa Y., Okuyama T., Shinoda T., Isobe T.;			
RT	*Covalent structure of bovine brain calreticulin.*;			
RL	Biochem. J. 298:435-442(1994).			
CC	!- FUNCTION: THIS PROTEIN BINDS CALCIUM. THERE ARE BOTH HIGH AND LOW AFFINITY CALCIUM-BINDING SITES.			
CC	!- SUBUNIT: MONOMER.			
CC	!- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM LUMEN.			
CC	!- SIMILARITY: BELONGS TO THE CALRETICULIN FAMILY.			
DR	InterPro: IPR001580; Calreticulin.			
DR	InterPro: IPR000886; ER-target.			
DR	Pfam: PF00262; calreticulin; 1.			
DR	PRINTS: PR00626; CALRETICULIN.			
DR	ProDom: PD001866; Calreticulin; 1.			
DR	PROSITE: PS00014; ER-TARGET; 1.			
DR	PROSITE: PS00803; CALRETICULIN_1; 1.			
DR	PROSITE: PS00804; CALRETICULIN_2; 1.			
KW	Endoplasmic reticulum; Calcium-binding; Repeat; Glycoprotein.			
FT	DOMAIN 1 180 N-DOMAIN.			
FT	DOMAIN 181 291 P-DOMAIN.			
FT	DOMAIN 292 400 C-DOMAIN.			
FT	DOMAIN 174 238 4 X APPROXIMATE REPEATS.			
FT	REPEAT 174 185 1-1.			
FT	REPEAT 193 204 1-2.			
FT	REPEAT 210 221 1-3.			
FT	REPEAT 227 238 1-4.			
FT	DOMAIN 242 280 3 X APPROXIMATE REPEATS.			
FT	REPEAT 242 252 2-1.			
FT	REPEAT 256 266 2-2.			
FT	REPEAT 270 280 2-3.			
FT	DOMAIN 334 390 ASP/GLU/LYS-RICH.			
FT	DISULFID 120 146 N-LINKED (GLCNAC. . .).			
FT	CARBOHYD 162 162 PREVENT SECRETION FROM ER (POTENTIAL).			
FT	SITE 397 400			
SQ	SEQUENCE 400 AA; 46381 MW; 7D4B68DFC689EEF1 CRC64;			

34	49	32.5	877	1	DPOL_BACCA
35	48.5	32.1	359	1	MLTA_BUCAL
36	48.5	32.1	1766	1	RPB1_TRYBB
37	48.5	32.1	1766	1	RPB2_TRYBB
38	47.5	31.5	619	1	CALX_CAEEL
39	47	31.1	170	1	Y887_MYCTU
40	47	31.1	273	1	FGG_STRMU
41	47	31.1	490	1	PURA_ARATH
42	47	31.1	1088	1	NCA1_XENLA
43	47	31.1	1092	1	NCA2_XENLA
44	46.5	30.8	334	1	CHI3_TOBAC
45	46.5	30.8	551	1	CALX_PEA

Q04957	bacillus ca
P57531	buchnera ap
P17545	trypanosoma
P17546	trypanosoma
P34652	caenorhabdi
Q10548	mycobacteri
P55045	streptococc
Q96529	arabidopsis
P16170	xenopus lae
P36335	xenopus lae
P29059	nicotiana t
O82709	pisum sativ

Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGPGTKKVVHVFYKGNVINKDIRC 27
 DB 120 CGPGTKKVVHVFYKGNVINKDIRC 146

RESULT 2
 CRTC_MOUSE
 ID CRTC_MOUSE STANDARD; PRT; 416 AA.
 AC P14211;
 DT 01-JAN-1990 (Rel. 13, Created)
 DT 01-JAN-1990 (Rel. 13, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE CALRETICULIN PRECURSOR (CRP55) (CALREGULIN) (HACBP) (ERP60).
 GN CALR.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID:10090;
 RN [1]
 RN SEQUENCE FROM N.A., AND SEQUENCE OF 18-48 AND 129-161.
 RP STRAIN-BALB/C; TISSUE-Liver;
 RC MEDLINE-90059955; PubMed 2583110;
 RA Smith M.J., Koch G.L.E.;
 RT "Multiple zones in the sequence of calreticulin (CRP55, calregulin,
 RT HACBP), a major calcium binding ER/SR protein.";
 RL EMBO J. 8:3581-3586(1989).
 RN [2]
 RN SEQUENCE FROM N.A.
 RX MEDLINE-93013037; PubMed 1398135;
 RA Mazzarella R.A., Gold P., Cunningham M., Green M.;
 RT "Determination of the sequence of an expressible cDNA clone encoding
 RT Fkp60/calregulin by the use of a novel nested set method.";
 RL Gene 120:217-225(1992).
 RN [3]
 RN SEQUENCE OF 18-38.
 RP TISSUE Fibroblast;
 RC MEDLINE-95009907; PubMed 7523108;
 RA Merrick B.A., Patterson R.M., Wichter L.L., He C., Selkirk J.K.;
 RT "Separation and sequencing of familial and novel murine proteins
 RT using preparative two-dimensional gel electrophoresis.";
 RL Electrophoresis 15:735-745(1994).
 CC -1- FUNCTION: THIS PROTEIN BINDS CALCIUM. THERE ARE BOTH HIGH AND
 CC LOW AFFINITY CALCIUM-BINDING SITES.
 CC -1- SURUNIT: MONOMER (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM LUMEN.
 CC -1- SIMILARITY: BELONGS TO THE CALRETICULIN FAMILY.
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 CC EMBL; X14926; CAA33053.1; -;
 CC EMBL; M92988; AAA37569.1; -;
 CC PIR; S06763; S06763.
 CC PIR; JC1444; JC1444.
 CC SWISS-2DPAGE; P14211; MOUSE.
 CC MCD; MGI:88252; Calr.
 CC InterPro; IPR001580; Calreticulin.
 CC InterPro; IPR000886; ER-target.
 CC Pfam; PF00262; calreticulin; 1.
 CC PRINTS; P000626; CALRETICULIN.
 CC ProDom; PD001866; Calreticulin; 1.
 CC PROSITE; PS00014; ER-TARGET; 1.
 CC PROSITE; PS00803; CALRETICULIN_1; 1.
 CC PROSITE; PS00804; CALRETICULIN_2; 1.
 CC PROSITE; PS00805; CALRETICULIN-REPEAT; 3.
 CC Endoplasmic reticulum; Calcium-binding; Repeat; Signal.

FT SIGNAL 1 17
 FT CHAIN 18 416
 FT DOMAIN 18 197
 FT DOMAIN 198 308
 FT DOMAIN 309 416
 FT DOMAIN 191 255
 FT REPEAT 191 202
 FT REPEAT 210 221
 FT REPEAT 227 238
 FT REPEAT 244 255
 FT DOMAIN 259 297
 FT REPEAT 259 269
 FT REPEAT 273 283
 FT REPEAT 287 297
 FT DOMAIN 351 407
 FT DISULFID 137 163
 FT SITE 413 416
 SQ SEQUENCE 416 AA; 47994 MW; 24C03B00913408D8 CRC64;

Query Match 100.0%; Score 151; DB 1; Length 416;
 Best Local Similarity 100.0%; Pred. No. 2.5e-14;
 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGPGTKKVVHVFYKGNVINKDIRC 27
 DB 137 CGPGTKKVVHVFYKGNVINKDIRC 163

RESULT 3
 CRTC_RAT
 ID CRTC_RAT STANDARD; PRT; 416 AA.
 AC P18418; P10452;
 DT 01-MAR-1989 (Rel. 10, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE CALRETICULIN PRECURSOR (CRP55) (CALREGULIN) (HACBP) (ERP60) (CALBP)
 DE (CALCIUM-BINDING PROTEIN 3) (CABP3).
 GN CALR.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID:10116;
 RN [1]
 RN SEQUENCE FROM N.A.
 RP STRAIN-SPRAGUE-DAWLEY; TISSUE-Brain cortex;
 RX MEDLINE-90370496; PubMed-2395661;
 RA Murthy K.K., Banville D., Srikant C.B., Carrier F., Bell A.,
 RA Holmes C., Patel V.C.;
 RT "Structural homology between the rat calreticulin gene product and
 RT the Onchocerca volvulus antigen Ral-1.";
 RL Nucleic Acids Res. 18:4933-4933(1990).
 RN [2]
 RN SEQUENCE FROM N.A.
 RP STRAIN-SPRAGUE-DAWLEY;
 RX MEDLINE-93202172; PubMed-8453984;
 RA Nakamura M., Moriya M., Baba T., Michikawa Y., Yamanobe T., Arai K.,
 RA Okinaga S., Kobayashi T.;
 RT "An endoplasmic reticulum protein, calreticulin, is transported into
 RT the acrosome of rat sperm.";
 RL Exp. Cell Res. 205:101-110(1993).
 RN [3]
 RN SEQUENCE FROM N.A.
 RP STRAIN-SPRAGUE-DAWLEY;
 RX MEDLINE-95181573; PubMed-7876339;
 RA Soenichsen B., Fuellekrug J., van Nguyen P., Diekmann W.,
 RA Robinson D.G., Mieskes G.;
 RT "Retention and retrieval: both mechanisms cooperate to maintain
 RT calreticulin in the endoplasmic reticulum.";
 RL J. Cell Sci. 107:2705-2717(1994).
 RN [4]
 RN SEQUENCE OF 270-358 FROM N.A.
 RP STRAIN-SPRAGUE-DAWLEY;

RA Lone Y.C., Bailly A., Latruffe N.;
 RL Submitted (DEC-1988) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RP SEQUENCE OF 18-29.
 RX MEDLINE=91054414; PubMed=2241926;
 RA Treves S., de Mattei M., Lanfredi M., Villa A., Green N.M.,
 RA MacLennan D.H., Meldolesi J., Pozzan T.;
 RT "Calreticulin is a candidate for a calsequestrin-like function in
 RT Ca2(+)-storage compartments (calcosomes) of liver and brain.";
 RL Biochem. J. 271:473-480(1990).
 RN [6]
 RP SEQUENCE OF 18-32.
 RC STRAIN=SPRAGUE-DAWLEY; TISSUE=Testis;
 RX MEDLINE=92360010; PubMed=1497655;
 RA Nakamura M., Michikawa Y., Baba T., Okinaga S., Arai K.;
 RT "Calreticulin is present in the acrosome of spermatids of rat
 RT testis.";
 RL Biochem. Biophys. Res. Commun. 186:668-673(1992).
 RN [7]
 RP SEQUENCE OF 18-32.
 RC STRAIN=LEC; TISSUE=Liver;
 RX MEDLINE=94072621; PubMed=8251535;
 RA Yokoi T., Nagayama S., Kajiura R., Kawaguchi Y., Horiuchi R.,
 RA Kametaki T.;
 RT "Identification of protein disulfide isomerase and calreticulin as
 RT autoimmune antigens in LEC strain of rats.";
 RL Biochim. Biophys. Acta 1158:339-344(1993).
 CC -!- FUNCTION: THIS PROTEIN BINDS CALCIUM. THERE ARE BOTH HIGH AND
 CC LOW AFFINITY CALCIUM-BINDING SITES.
 CC -!- SUBUNIT: MONOMER (BY SIMILARITY).
 CC -!- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM LUMEN.
 CC -!- SIMILARITY: BELONGS TO THE CALRETICULIN FAMILY.
 CC -!- CAUTION: WAS ORIGINALLY (REF.2) THOUGHT TO BE D-BETA-
 CC HYDROXYBUTYRATE DEHYDROGENASE.
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 DR EMBL; D78308; BA011345.1; -;
 DR EMBL; X53363; CAA37446.1; -;
 DR EMBL; X13702; CAA31987.1; ALT_SEQ.
 DR EMBL; X79327; CAA55890.1; -;
 DR PIR; S04867; S04867.
 DR PIR; S11205; S11205.
 DR PIR; S13045; S13045.
 DR PIR; A49176; A49176.
 DR PIR; S45036; S45036.
 DR PIR; JH0819; JH0819.
 DR InterPro; IPR001580; Calreticulin.
 DR InterPro; IPR000886; ER_target.
 DR Pfam; PF00262; calreticulin; 1.
 DR PRINTS; PR00626; CALRETICULIN.
 DR ProDom; PD001866; Calreticulin; 1.
 DR PROSITE; PS00014; ER_TARGET; 1.
 DR PROSITE; PS00803; CALRETICULIN_1; 1.
 DR PROSITE; PS00804; CALRETICULIN_2; 1.
 DR PROSITE; PS00805; CALRETICULIN_REPEAT; 3.
 KW Endoplasmic reticulum; Calcium-binding; Repeat; Signal.
 FT SIGNAL 1 17
 FT CHAIN 18 416 CALRETICULIN.
 FT DOMAIN 18 197 N-DOMAIN.
 FT DOMAIN 198 308 P-DOMAIN.
 FT DOMAIN 309 416 C-DOMAIN.
 FT DOMAIN 191 255 4 X APPROXIMATE REPEATS.
 FT REPEAT 191 202 1-1.
 FT REPEAT 210 221 1-2.
 FT REPEAT 227 238 1-3.
 FT REPEAT 244 255 1-4.

FT DOMAIN 259 297 3 X APPROXIMATE REPEATS.
 FT REPEAT 259 269 2-1.
 FT REPEAT 273 283 2-2.
 FT REPEAT 287 297 2-3.
 FT DOMAIN 351 407 ASP/GLU/LYS-RICH.
 FT DISULFID 137 163 BY SIMILARITY.
 FT SITE 413 416 PREVENT SECRETION FROM ER.
 SQ SEQUENCE. 416 AA; 47995 MW; 2E6713CED31A2970 CRC64;
 Query Match 100.0%; Score 151; DB 1; Length 416;
 Best Local Similarity 100.0%; Pred. No. 2.5e-14;
 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CGPGTKKHVIFNYKGNVLINKDIRC 27
 Db 137 CGPGTKKHVIFNYKGNVLINKDIRC 163
 RESULT 4
 CRTC_HUMAN
 ID CRTC_HUMAN STANDARD; PRT; 417 AA.
 AC P27797;
 DT 01-AUG-1992 (Rel. 23, Created)
 DT 01-AUG-1992 (Rel. 23, Last sequence update)
 DT 20-AUG-2001 (Rel. 40, Last annotation update)
 DE CALRETICULIN PRECURSOR (CRP55) (CALREGULIN) (HACBP) (ERP60) (52 KDA
 DE RIBONUCLEOPROTEIN AUTOANTIGEN RO/SS-A).
 GN CALR OR CRTC.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=92013129; PubMed=1919005;
 RA Rokeach L.A., Haselby J.A., Melloy J.F., Smeenk R.J., Unnasch T.R.,
 RA Greene B.M., Hoch S.O.;
 RT "Characterization of the autoantigen calreticulin.";
 RL J. Immunol. 147:3031-3039(1991).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=90237213; PubMed=2332496;
 RA McCauliffe D.P., Lux F.A., Lieu T.S., Sanz I., Hanke J., Newkirk M.M.,
 RA Bachinski L.L., Itoh Y., Siciliano M.J., Reichlin M., Sontheimer R.D.,
 RA Capra J.D.;
 RT "Molecular cloning, expression, and chromosome 19 localization of a
 RT human Ro/SS-A autoantigen.";
 RL J. Clin. Invest. 85:1379-1391(1990).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=92129342; PubMed=1733953;
 RA McCauliffe D.P., Yang Y.S., Wilson J., Sontheimer R.D., Capra J.D.;
 RT "The 5'-flanking region of the human calreticulin gene shares
 RT homology with the human GRP78, GRP94, and protein disulfide isomerase
 RT promoters.";
 RL J. Biol. Chem. 267:2557-2562(1992).
 RN [4]
 RP SEQUENCE FROM N.A.
 RA Lamerdin J., McCreedy P., Stilwagen S., Ramirez M., Carrano A.;
 RL Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RP SEQUENCE OF 18-36.
 RX MEDLINE=92002034; PubMed=1911778;
 RA Rojiani M.V., Finlay B.B., Gray V., Dedhar S.;
 RT "In vitro interaction of a polypeptide homologous to human Ro/SS-A
 RT antigen (calreticulin) with a highly conserved amino acid sequence in
 RT the cytoplasmic domain of integrin alpha subunits.";
 RL Biochemistry 30:9859-9866(1991).
 RN [6]
 RP SEQUENCE OF 18-32.
 RX MEDLINE=90380058; PubMed=2400400;
 RA Krause K.H., Simmerman H.K.B., Jones L.R., Campbell K.P.;

Sequence similarity of calreticulin with a Ca2(+)-binding protein that co-purifies with an Ins(1,4,5)P3-sensitive Ca2+ store in HL-60 cells.;
 RL Biochem. J. 270:545-548(1990).
 [17]

RN SEQUENCE OF 18-28.

RP TISSUE Liver;
 RX MEDLINE 93162045; PubMed 1286669;
 RA Hochstrasser D.F., Frutiger S., Paquet N., Bairoch A., Ravier F.,
 RA Pasquali C., Sanchez J.-C., Tissot J.-D., Bjellqvist B., Vargas R.,
 RA Appel R.D., Hughes G.J.;
 RA "Human liver protein map: a reference database established by
 microsequencing and gel comparison.*";
 KT Electrophoresis 13:982-1001(1992).
 RL [18]

RN PARTIAL SEQUENCE OF 25-34; 56-62; 208-221 AND 273-278.

RP TISSUE Keratinocytes;
 RX MEDLINE 93162043; PubMed 1286667;
 RA Rasmussen H.H., van Damme J., Puyse M., Gesser B., Cells J.E.,
 RA Vandekerckhove J.;
 RA "Microsequences of 145 proteins recorded in the two-dimensional gel
 protein database of normal human epidermal keratinocytes.*";
 KT Electrophoresis 13:960-969(1992).
 RL [19]

RN SEQUENCE OF 18-26.

RP TISSUE-Colon carcinoma;
 RX MEDLINE 97295306; PubMed 9150948;
 RA Ji H., Reid G.E., Moritz R.U., Eddes J.S., Burgess A.W., Simpson R.J.;
 RA "A two-dimensional gel database of human colon carcinoma proteins.*";
 RL Electrophoresis 18:605-613(1997).
 CC -!- FUNCTION: THIS PROTEIN BINDS CALCIUM. THERE ARE BOTH HIGH AND
 CC LOW AFFINITY CALCIUM-BINDING SITES.

CC -!- SUBUNIT: MONOMER (BY SIMILARITY)

CC -!- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM LUMEN.

CC -!- SIMILARITY: BELONGS TO THE CALRETICULIN FAMILY.

CC -!- CAUTION: WAS ORIGINALLY (REF.2) THOUGHT TO BE THE RO AUTOANTIGEN.

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CC EMBL; H84739; AAA51916.1; -

CC EMBL; M12294; AAA76582.1; -

CC EMBL; AD000092; BAB51176.1; -

CC PIR; A37047; A37047.

CC PIR; S11475; S11475.

CC PIR; A42330; A42330.

CC PIR; A46452; A46452.

CC SWISS-2DPAGE; P27797; HUMAN.

CC Aarhus/Ghent-2DPAGE; 9401; IEF.

CC HSC-2DPAGE; P27797; HUMAN.

CC MIM; 109091; -

CC InterPro; IPR001580; Calreticulin.

CC InterPro; IPR000886; ER-target.

CC Pfam; PF00462; calreticulin; 1.

CC PRINTS; P00626; CALRETICULIN.

CC ProDom; PD001866; Calreticulin; 1.

CC PROSITE; PS00014; ER-TARGET; 1.

CC PROSITE; PS00803; CALRETICULIN; 1.

CC PROSITE; PS00804; CALRETICULIN; 2; 1.

CC PROSITE; PS00805; CALRETICULIN-REPEAT; 3.

KW Endoplasmic reticulum; Calcium-binding; Repeat; Signal.

FT SIGNAL 1 17

FT CHAIN 18 417

FT CALRETICULIN.

FT DOMAIN 18 197

FT N-DOMAIN.

FT DOMAIN 198 308

FT P-DOMAIN.

FT DOMAIN 309 417

FT C-DOMAIN.

FT DOMAIN 191 255

FT 4 X APPROXIMATE REPEATS.

FT REPEAT 210 221 1-2.
 FT REPEAT 227 238 1-3.
 FT REPEAT 244 255 1-4.
 FT DOMAIN 259 297 3 X APPROXIMATE REPEATS.
 FT REPEAT 269 297 2-1.
 FT REPEAT 273 283 2-2.
 FT REPEAT 287 297 2-3.
 FT DOMAIN 351 408 ASP/GLU/LYS-RICH.
 FT DISULFID 137 163 BY SIMILARITY.
 FT SITE 414 417 PREVENT SECRETION FROM ER.
 FT CONFLICT 35 35 MISSING (IN REF. 3).
 SQ SEQUENCE 417 AA; 48141 MW; BC37C3C0F1054FB2 CRC64;

Query Match 100.0%; Score 151; DB 1; Length 417;
 Best local Similarity 100.0%; Pred. No. 2.5e-14;
 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGPGTKKHVHVFYKGNVINKDIRC 27

Db 137 CGPGTKKHVHVFYKGNVINKDIRC 163

RESULT 5

CRTC_RABIT STANDARD; PRT; 418 AA.
 ID CRTC_RABIT STANDARD; PRT; 418 AA.
 AC P15253;

DT 01-APR-1990 (Rel. 14, Created)

DT 01-APR-1990 (Rel. 14, Last sequence update)

DT 01-OCT-1996 (Rel. 34, Last annotation update)

DE CALRETICULIN PRECURSOR (CRP55) (CALREGULIN) (HACBP) (ERP60).
 GN CALR

OS Oryctolagus cuniculus (Rabbit).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.

OX NCBI_TaxID:9986;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE:Slow-twitch skeletal muscle;

RX MEDLINE 90094320; PubMed-260080;

RA Fliegel L., Burns K., MacLennan D.H., Reithmeier R.A.F., Michalak M.;

RT "Molecular cloning of the high affinity calcium-binding protein

(calreticulin) of skeletal muscle sarcoplasmic reticulum.*";

RL J. Biol. Chem. 264:21522-21528(1989).

RN [2]

RP SEQUENCE FROM N.A.

RC TISSUE:Fast-twitch skeletal muscle;

RX MEDLINE 91282795; PubMed-2059224;

RA Fliegel L., Michalak M.;

RT "Fast-twitch and slow-twitch skeletal muscles express the same

isoform of calreticulin.*";

RL Biochem. Biophys. Res. Commun. 177:979-984(1991).

RN [3]

RP SEQUENCE OF 18-36.

RX MEDLINE 91054414; PubMed-2241926;

RA Treves S., de Mattei M., Lanfredi M., Villa A., Green N.M.,

RA MacLennan D.H., Meldolesi J., Pozzan T.;

RT "Calreticulin is a candidate for a calsequestrin-like function in

Ca2(+)-storage compartments (calciosomes) of liver and brain.*";

RL Biochem. J. 271:473-480(1990).

RN [4]

RP SEQUENCE OF 18-46.

RX MEDLINE 91201375; PubMed-2016321;

RA Milner R.E., Baksh S., Shemanko C., Carpenter M.R., Smillie L.,

RA Vance J.E., Opas M., Michalak M.;

RT "Calreticulin, and not calsequestrin, is the major calcium binding

protein of smooth muscle sarcoplasmic reticulum and liver endoplasmic

reticulum.*";

RL J. Biol. Chem. 266:7155-7165(1991).

RN [5]

RP PARTIAL SEQUENCE.

RT TISSUE Lung;

RX MEDLINE 92002038; PubMed-1911780;

RA Guan S., Fallick A.M., Williams D.E., Cashman J.R.;
 RT "Evidence for complex formation between rabbit lung flavin-containing
 RL monooxygenase and calreticulin.";
 CC Biochemistry 30:9892-9900(1991).
 CC -!- FUNCTION: THIS PROTEIN BINDS CALCIUM. THERE ARE BOTH HIGH AND
 CC LOW AFFINITY CALCIUM-BINDING SITES.
 CC -!- SUBUNIT: MONOMER (BY SIMILARITY).
 CC -!- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM LUMEN.
 CC -!- SIMILARITY: BELONGS TO THE CALRETICULIN FAMILY.
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 CC -----
 DR EMBL: J05138; AAA31188.1; -;
 DR PIR: A34154; A34154.
 DR PIR: C33208; C33208.
 DR PIR: D33208; D33208.
 DR PIR: E33208; E33208.
 DR PIR: F33208; F33208.
 DR PIR: S13046; S13046.
 DR PIR: S13047; S13047.
 DR InterPro: IPR001580; Calreticulin.
 DR InterPro: IPR000886; ER_target.
 DR Pfam: PF00262; calreticulin.1.
 DR PRINTS: PR00626; CALRETICULIN.
 DR PRODOM: PD001866; Calreticulin; 1.
 DR PROSITE: PS00014; ER_TARGET; 1.
 DR PROSITE: PS00803; CALRETICULIN_1; 1.
 DR PROSITE: PS00804; CALRETICULIN_2; 1.
 DR PROSITE: PS00805; CALRETICULIN_REPEAT; 3.
 KW Endoplasmic reticulum; Calcium-binding; Repeat; Signal.
 FT SIGNAL 1 17
 FT CHAIN 18 418 CALRETICULIN.
 FT DOMAIN 18 197 N-DOMAIN.
 FT DOMAIN 198 308 P-DOMAIN.
 FT DOMAIN 309 418 C-DOMAIN.
 FT DOMAIN 191 255 4 X APPROXIMATE REPEATS.
 FT REPEAT 191 202 1-1.
 FT REPEAT 210 221 1-2.
 FT REPEAT 227 238 1-3.
 FT REPEAT 244 255 1-4.
 FT DOMAIN 259 297 3 X APPROXIMATE REPEATS.
 FT REPEAT 259 269 2-1.
 FT REPEAT 273 283 2-2.
 FT REPEAT 287 297 2-3.
 FT DOMAIN 351 408 ASP/GLU/LYS-RICH.
 FT DISULFID 137 163 BY SIMILARITY.
 FT SITE 415 418 PREVENT SECRETION FROM ER.
 FT VARIANT 35 35 E -> D.
 FT CONFLICT 90 90 P -> T (IN REF. 5).
 SQ SEQUENCE 418 AA; 48275 MW; B6082B689DC763A6 CRC64;

Query Match 100.0%; Score 151; DB 1; Length 418;
 Best Local Similarity 100.0%; Pred. No. 2.6e-14;
 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 CGPGTKKVVHVFNYKGNVINKNDIRC 27
 |||||||||||||||||||||||||||||
 Db 137 CGPGTKKVVHVFNYKGNVINKNDIRC 163

RESULT 6
 ID CRT2_BOVIN STANDARD; PRT; 421 AA.
 AC P42918;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)

DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE CALRETICULIN, BRAIN ISOFORM 2 PRECURSOR (CRP55) (CALREGULIN) (HACBP).
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 OX NCBI_taxid=9913;
 RN [1]
 RC SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=93385184; PubMed=8373827;
 RA Liu N., Fine R.E., Johnson R.J.;
 RT "Comparison of cDNAs from bovine brain coding for two isoforms of
 RT calreticulin.";
 RL Biochim. Biophys. Acta 1202:70-76(1993).
 CC -!- FUNCTION: THIS PROTEIN BINDS CALCIUM. THERE ARE BOTH HIGH AND
 CC LOW AFFINITY CALCIUM-BINDING SITES.
 CC -!- SUBUNIT: MONOMER (BY SIMILARITY).
 CC -!- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM LUMEN.
 CC -!- SIMILARITY: BELONGS TO THE CALRETICULIN FAMILY.
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 CC -----
 DR EMBL: L13462; AAC37307.1; -;
 DR InterPro: IPR001580; Calreticulin.
 DR InterPro: IPR000886; ER_target.
 DR Pfam: PF00262; calreticulin.1.
 DR PRINTS: PR00626; CALRETICULIN.
 DR PRODOM: PD001866; Calreticulin; 1.
 DR PROSITE: PS00014; ER_TARGET; 1.
 DR PROSITE: PS00803; CALRETICULIN_1; 1.
 DR PROSITE: PS00804; CALRETICULIN_2; 1.
 DR PROSITE: PS00805; CALRETICULIN_REPEAT; 3.
 KW Endoplasmic reticulum; Calcium-binding; Repeat; Signal.
 FT SIGNAL 1 34 POTENTIAL.
 FT CHAIN 35 421 CALRETICULIN, BRAIN ISOFORM 2.
 FT DOMAIN 35 201 N-DOMAIN.
 FT DOMAIN 202 312 P-DOMAIN.
 FT DOMAIN 313 421 C-DOMAIN.
 FT DOMAIN 195 259 4 X APPROXIMATE REPEATS.
 FT REPEAT 195 206 1-1.
 FT REPEAT 214 225 1-2.
 FT REPEAT 231 242 1-3.
 FT REPEAT 248 259 1-4.
 FT DOMAIN 263 301 3 X APPROXIMATE REPEATS.
 FT REPEAT 263 273 2-1.
 FT REPEAT 277 287 2-2.
 FT REPEAT 291 301 2-3.
 FT DOMAIN 366 411 ASP/GLU/LYS-RICH.
 FT DISULFID 141 167 BY SIMILARITY.
 FT CARBOHYD 183 183 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT SITE 418 421 PREVENT SECRETION FROM ER.
 SQ SEQUENCE 421 AA; 48812 MW; 0257E959F71528BC CRC64;

Query Match 100.0%; Score 151; DB 1; Length 421;
 Best Local Similarity 100.0%; Pred. No. 2.6e-14;
 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 CGPGTKKVVHVFNYKGNVINKNDIRC 27
 |||||||||||||||||||||||||||||
 Db 141 CGPGTKKVVHVFNYKGNVINKNDIRC 167

RESULT 7
 ID CRTC_DROME STANDARD; PRT; 406 AA.

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AC P29413; Q9VHA3;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-OCT-1993 (Rel. 27, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE CALRETICULIN PRECURSOR (CRP55) (CALREGLIN) (HACBP).
GN CRC OR CG9429.
OS Drosophila melanogaster (Fruit fly).
OC Pterygota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID 7227;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE 93208374; PubMed 1296819;
RA Smith M.J.;
RT "Nucleotide sequence of a Drosophila melanogaster gene encoding a
KL calreticulin homologue.";
RN [2]
RP DNA Seq. 3:247-250(1992).
RP SEQUENCE FROM N.A.
RC STRAIN-BERKELEY;
RX MEDLINE-20196006; PubMed-10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amaratunga P.G., Scher S.E., Li P.W., Hoskins R.A., Galie R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Vandal M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champ M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Abuyani A., An H.-J., Andrews-Frannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Rurtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Flossler C., Gabriellian A.E., Garq N.S., Gelbart W.M., Glasser K.,
RA Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattai B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Morkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Paluzzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reibert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Klanos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner K., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin C.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RL Science 287:2185-2195(2000).
RN [3]
RP SEQUENCE OF 91-124 AND 182-220.
RX MEDLINE 90307981; PubMed 2365822;
RA McCaulliffe D.P., Zappi E., Lieu T.S., Michalak M., Sontheimer R.D.,
RA Capra J.D.;
RT "A human Ro/SS-A autoantigen is the homologue of calreticulin and is
KT highly homologous with onchocercal RAL-1 antigen and an aplysia
KT 'memory molecule'.";
RL J. Clin. Invest. 86:332-335(1990).
CC -!- FUNCTION: THIS PROTEIN BINDS CALCIUM. THERE ARE BOTH HIGH AND
CC LOW AFFINITY CALCIUM-BINDING SITES.
CC -!- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM LUMEN.
CC -!- SIMILARITY: BELONGS TO THE CALRETICULIN FAMILY.

```

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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; X64461; CAA45791.1; -.
CC EMBL; AE003683; AAF54416.1; -.
CC DR PIR; A37158; A37158.
CC DR FlyBase; FBgn0005585; Crc.
CC DR InterPro; IPR001580; Calreticulin.
CC DR InterPro; IPR000886; ER_target.
CC DR Pfam; PF00262; calreticulin; 1.
CC DR PRINTS; PR00626; CALRETICULIN.
CC DR ProDom; PD001866; Calreticulin; 1.
CC DR PROSITE; PS00014; ER_TARGET; 1.
CC DR PROSITE; PS00803; CALRETICULIN_1; 1.
CC DR PROSITE; PS00804; CALRETICULIN_2; 1.
CC DR PROSITE; PS00805; CALRETICULIN_REPEAT; 3.
CC KW Endoplasmic reticulum; calcium-binding; Repeat; Signal.
CC FT SIGNAL 1 17 POTENTIAL.
CC FT CHAIN 18 406 CALRETICULIN.
CC FT CONFLICT 107 107 G -> A (IN REF. 3).
CC FT CONFLICT 184 184 V -> L (IN REF. 3).
CC FT SEQUENCE 406 AA; 46808 MW; 65D72C69D0BE427 CRC64;
CC SQ

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Query Match 88.7%; Score 134; DB 1; Length 406;
Best Local Similarity 88.9%; Pred. No. 6.7e-12;
Matches 24; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 CGPGTKKHVIFNYKGNVLNKDIRC 27
Db 137 CGPGTKKHVIFSYKGNHLISKDIRC 163
|||||
CGPGTKKHVIFNYKGNVLNKDIRC 27
CGPGTKKHVIFSYKGNHLISKDIRC 163

RESULT 8
RAL1_ONCVO STANDARD; PRT; 388 AA.
AC P11012;
DT 01-JUL-1989 (Rel. 11, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE RAL-1 PROTEIN PRECURSOR (41 KDA LARVAL ANTIGEN).
GN RAL1.
OS Onchocerca volvulus.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Filarioidea;
OC Onchocercidae; Onchocerca.
OX NCBI_TaxID:6282;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-94341871; PubMed-7520419;
RA Rokeach L.A., Zimmerman P.A., Unnasch T.R.;
RT "Epitopes of the Onchocerca volvulus RAL1 antigen, a member of the
RT calreticulin family of proteins, recognized by sera from patients
RT with onchocerciasis.";
RL Infect. Immun. 62:3696-3704(1994).
RN [2]
RP SEQUENCE OF 53-388 FROM N.A.
RX MEDLINE-88273584; PubMed 2455736;
RA Unnasch T.R., Gallin M.Y., Soboslay P.T., Ertmann K.D., Greene B.M.;
RT "Isolation and characterization of expression cDNA clones encoding
RT antigens of Onchocerca volvulus infective larvae.";
RL J. Clin. Invest. 82:262-269(1988).
CC -!- SIMILARITY: BELONGS TO THE CALRETICULIN FAMILY.
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DR InterPro; IPR001580; Calreticulin.
DR InterPro; IPR000886; ER_target.
DR Pfam; PF00262; calreticulin; 1.
DR PRINTS; PR00626; CALRETICULIN.
DR ProDom; PD001866; Calreticulin; 1.
DR PROSITE; PS00014; ER_TARGET; 1.
DR PROSITE; PS00803; CALRETICULIN_1; 1.
DR PROSITE; PS00804; CALRETICULIN_2; 1.
DR PROSITE; PS00805; CALRETICULIN_REPEAT; 2.
KW Endoplasmic reticulum; Calcium-binding; Repeat; Signal; Glycoprotein.
FT SIGNAL 1 25 POTENTIAL.
FT CHAIN 26 416 CALRETICULIN.
FT CARBOHYD 57 57 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 157 157 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT SITE 413 416 PREVENT SECRETION FROM ER (POTENTIAL).
SQ SEQUENCE 416 AA: 48136 MW; 565FEC3489F77CA7 CRC64;

Query Match 60.9%; Score 92; DB 1; Length 416;
Best Local Similarity 63.0%; Pred. No. 7; le-06;
Matches 17; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

OY 1 CGPGTKKHVIFNYKGNVLINKDIRC 27
II IIIII IIII I I I I I I
DB 143 CGYSTKKVHAIFNYDTHLKKDVP 169

RESULT 13

CRT3_ARATH
ID CRT3_ARATH STANDARD; PRT: 424 AA.
AC 004153; Q9SJE7;
DT 20-AUG-2001 (Rel. 40, Created)
DT 20-AUG-2001 (Rel. 40, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE CALRETICULIN 3 PRECURSOR.
GN CRT3 OR T27G7.13.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97303616; PubMed=9159940;
RA Nelson D.E., Glaunsinger B., Bohnert H.J.;
RT "Abundant accumulation of the calcium-binding molecular chaperone
calreticulin in specific floral tissues of Arabidopsis thaliana.";
RL Plant Physiol. 114:29-37(1997).
RN [2]

RP SEQUENCE FROM N.A.
RA Shinn P., Brooks S., Buehler E., Chao Q., Johnson-Hopson C., Khan S.,
RA Kim C., Altafi H., Bei O., Chin C., Chiou J., Choi E., Conn L.,
RA Conway A., Gonzales A., Hansen N., Howing B., Koo T., Lam B., Lee J.,
RA Lenz C., Li J., Liu A., Liu K., Liu S., Mukharsky N., Nguyen M.,
RA Palm C., Pham P., Sakano H., Schwartz J., Southwick A., Thaveri A.,
RA Toriumi M., Vaysberg M., Yu G., Federspiel N.A., Theologis A.,
RA Ecker J.R.;
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: THIS PROTEIN BINDS CALCIUM. THERE ARE BOTH HIGH AND
CC LOW AFFINITY CALCIUM-BINDING SITES (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM LUMEN (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE CALRETICULIN FAMILY.
CC -----

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CC or send an email to license@isb-sib.ch).
CC -----

DR EMBL; U66345; AAC49697.1; .
DR EMBL; AC006932; AAF22902.1; ALT_SEQ.

DR Mendel; 16507; Arath;1166;16507.
DR InterPro; IPR001580; Calreticulin.
DR InterPro; IPR000886; ER_target.
DR Pfam; PF00262; calreticulin; 1.
DR PRINTS; PR00626; CALRETICULIN.
DR ProDom; PD001866; Calreticulin; 1.
DR PROSITE; PS00014; ER_TARGET; 1.
DR PROSITE; PS00803; CALRETICULIN_1; 1.
DR PROSITE; PS00804; CALRETICULIN_2; 1.
DR PROSITE; PS00805; CALRETICULIN_REPEAT; 2.
KW Endoplasmic reticulum; Calcium-binding; Repeat; Signal; Glycoprotein.
FT SIGNAL 1 28 POTENTIAL.
FT CHAIN 29 424 CALRETICULIN 3.
FT CARBOHYD 97 97 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT SITE 421 424 PREVENT SECRETION FROM ER (POTENTIAL).
FT CONFLICT 279 279 F -> S (IN REF. 2).
SQ SEQUENCE 424 AA: 49904 MW; 650E0A8342F0B97 CRC64;

Query Match 58.3%; Score 88; DB 1; Length 424;
Best Local Similarity 55.6%; Pred. No. 2; 7e-05;
Matches 15; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

OY 1 CGPGTKKHVIFNYKGNVLINKDIRC 27
II IIIII IIII I I I I I I
DB 146 CGTQTKKLHVIVSYQGQNPYIKKDLQC 172

RESULT 14

CRTC_PUJAR
ID CRTC_PUJAR STANDARD; PRT: 421 AA.
AC Q9XF98;
DT 20-AUG-2001 (Rel. 40, Created)
DT 20-AUG-2001 (Rel. 40, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE CALRETICULIN PRECURSOR.
OS Prunus armeniaca (Apricot).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids I; Rosales; Rosaceae; Prunus.
OX NCBI_TaxID=36596;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. BERGERON; TISSUE=Mesocarp, and Endocarp;
RA Mbeguie-A-Mbeguie D., Fills-Lycaon B.R.;
RT "Molecular cloning and nucleotide sequence of a calreticulin from
apricot (Prunus armeniaca cv. Bergeron).";
RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: THIS PROTEIN BINDS CALCIUM. THERE ARE BOTH HIGH AND
CC LOW AFFINITY CALCIUM-BINDING SITES (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM LUMEN (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE CALRETICULIN FAMILY.
CC -----

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CC or send an email to license@isb-sib.ch).
CC -----

DR EMBL; AFL34733; AAD32207.1; .

DR InterPro; IPR001580; Calreticulin.
DR InterPro; IPR000886; ER_target.
DR Pfam; PF00262; calreticulin; 1.
DR PRINTS; PR00626; CALRETICULIN.
DR ProDom; PD001866; Calreticulin; 1.
DR PROSITE; PS00014; ER_TARGET; 1.
DR PROSITE; PS00803; CALRETICULIN_1; 1.
DR PROSITE; PS00804; CALRETICULIN_2; 1.
DR PROSITE; PS00805; CALRETICULIN_REPEAT; 2.
KW Endoplasmic reticulum; Calcium-binding; Repeat; Signal; Glycoprotein.

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FT SIGNAL 1 22 POTENTIAL.
FT CHAIN 23 421 CALRETICULIN.
FT CARBOHYD 56 56 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 156 156 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT SITE 438 421 PREVENT SECRETION FROM ER (POTENTIAL).
SQ SEQUENCE 421 AA; 48416 MW; 4F5F94CBAA6C6690 CRC64;

Query Match 57.6%; Score 87; DB 1; Length 421;
Best Local Similarity 59.3%; Pred.No. 3.7e-05;
Matches 16; Conservative 1; Mismatches 10; Indels 0; Gaps 0;

QY 1 CGPGTKKHVIFNYKGNVLINKDIRC 27
II IIII I I I I I I I I I
DB 142 CGYSTKKVHAILNYNTNNLIKDDVPC 168

RESULT 15
CRT2_ARATH
ID CRT2_ARATH STANDARD; PRT; 424 AA.
AC Q38858; 080486; 004152;
DT 20-AUG-2001 (Rel. 40, Created)
DT 20-AUG-2001 (Rel. 40, Last sequence update)
DE CALRETICULIN 2 PRECURSOR.
GN CRT2 OR CRTL OR T12M4.8.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC Eurosid II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID:3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-CV. COLUMBIA;
RA Vysotskaya V.S., Schwartz J.R., Toriumi M., Yu G., Oji O., Kwan A.,
RA Liu S., Li J., Araujo R., Au M., Brendel V., Buehler E., Conway A.B.,
RA Conway A.R., Dewar K., Feng K., Kim C., Kurtz D., Li Y., Palm C.J.,
RA Shinn P., Sun H., Davis R.W., Ecker J.R., Federspiel N.A.,
RA Theologis A.
RL Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.
RN [2]
SQ SEQUENCE OF 1-174 FROM N.A.
RX MEDLINE 97303616; PubMed 9159940;
RA Nilsson D.E., Glaunsinger B., Bohnert H.J.;
RT "Abundant accumulation of the calcium-binding molecular chaperone
RT calreticulin in specific floral tissues of Arabidopsis thaliana.";
RL Plant Physiol. 114:29-37(1997).
RN [3]
SQ SEQUENCE OF 16-424 FROM N.A.
RC STRAIN-CV. LANDSBERG RECTA; TISSUE Flower;
RA Benedetti C.E., Turner J.G.;
RT "Nucleotide sequence of an Arabidopsis thaliana cDNA encoding a
RT protein homologous to plant and animal calreticulins.";
RL (In) Plant Gene Register PCR95-047.
CC -1- FUNCTION: THIS PROTEIN BINDS CALCIUM. THERE ARE BOTH HIGH AND
CC LOW AFFINITY CALCIUM-BINDING SITES (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM LUMEN (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE CALRETICULIN FAMILY.
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CC -----
CC EMBL; AC003114; AAC24083.1; ALT SEQ.
DR EMBL; U66344; AAC49696.1; ALT_INIT.
DR EMBL; U27698; AAA80652.1;
DR HSSP; P00268; 4RXN.
DR SWISS-2DPAGE; Q38858; ARATH.
DR Mende1; 6599; Arath; 1166; 6599.
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DR Mende1; 31147; Arath; 1166; 31147.
DR Mende1; 16506; Arath; 1166; 16506.
DR InterPro; IPR001580; Calreticulin.
DR InterPro; IPR000886; ER_target.
DR Pfam; PF00262; calreticulin; 1.
DR PRINTS; PR00626; CALRETICULIN.
DR ProDom; PD001866; Calreticulin; 1.
DR PROSITE; PS00014; ER_TARGET; 1.
DR PROSITE; PS00803; CALRETICULIN_1; 1.
DR PROSITE; PS00804; CALRETICULIN_2; 1.
DR PROSITE; PS00805; CALRETICULIN_REPEAT; 2.
KW Endoplasmic reticulum; Calcium-binding; Repeat; Signal; Glycoprotein;
KW Multigene family.
FT SIGNAL 1 22 POTENTIAL.
FT CHAIN 23 424 CALRETICULIN 2.
FT CARBOHYD 59 59 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT SITE 421 424 PREVENT SECRETION FROM ER (POTENTIAL).
FT CONFLICT 16 19 LVAI -> NSAR (IN REF. 3).
FT CONFLICT 155 155 G -> E (IN REF. 1).
FT CONFLICT 236 236 P -> T (IN REF. 3).
FT CONFLICT 408 408 V -> E (IN REF. 3).
SQ SEQUENCE 424 AA; 48084 MW; 514385EBAE810DD7 CRC64;

Query Match 57.6%; Score 87; DB 1; Length 424;
Best Local Similarity 59.3%; Pred.No. 3.8e-05;
Matches 16; Conservative 1; Mismatches 10; Indels 0; Gaps 0;

QY 1 CGPGTKKHVIFNYKGNVLINKDIRC 27
II IIII I I I I I I I I I
DB 140 CGYSTKKVHAILTYNGANHLIKDDVPC 166
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Search completed: January 9, 2002, 15:12:15
Job time: 657 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: January 9, 2002, 15:02:02 ; Search time 43.73 Seconds
(without alignments)
47.032 Million cell updates/sec

Title: US-09-828-000-5
Perfect score: 151
Sequence: 1 CGPGTKKHVIFNYKGNVLINKDIRC 27
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues
Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_68.*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	151	100.0	400	2 S43376	calreticulin, brai
2	151	100.0	416	1 S06763	calreticulin precu
3	151	100.0	416	2 JH0819	calreticulin precu
4	151	100.0	417	1 A37047	calreticulin precu
5	151	100.0	418	1 A34154	calreticulin precu
6	151	100.0	421	2 S36799	calreticulin precu
7	141	93.4	405	1 JH0795	calreticulin precu
8	134	88.7	406	2 A56637	calreticulin homol
9	125	82.8	419	2 S71343	calreticulin precu
10	121	80.1	336	2 A32507	41K larval antigen
11	120	79.5	384	2 S29130	calreticulin (clon
12	120	79.5	411	2 S29129	calreticulin precu
13	112	74.2	393	1 A48573	calreticulin autoa
14	96.5	63.9	395	2 S25851	calreticulin precu
15	92	60.9	416	2 T14554	calreticulin - bee
16	84	55.6	412	2 T05703	calreticulin - bar
17	84	55.6	415	2 T05705	calreticulin - bar
18	83	55.0	421	2 S58170	calreticulin precu
19	83	55.0	425	2 C96605	calreticulin (Ctrl
20	82	54.3	415	2 T10172	calreticulin - cas
21	80	53.0	422	2 T07841	probable calreticu
22	79	52.3	444	2 H86224	hypothetical prote
23	76	50.3	389	2 T03691	calreticulin - com
24	76	50.3	416	2 T16968	calreticulin call
25	54	35.8	720	2 T43854	helicase [imported
26	53	35.1	464	2 A53101	vitamin D3 hydroxy
27	53	35.1	764	2 F83161	pyocin protein PA3
28	52	34.4	1938	1 MNKWL	myosin heavy chain
29	51	33.8	560	2 S50439	hypothetical prote

30	51	33.8	725	1 IJMSNG	neural cell adhesi
31	51	33.8	761	1 IJHUNG	neural cell adhesi
32	51	33.8	853	1 IJBONC	neural cell adhesi
33	51	33.8	858	1 IJRTNC	neural cell adhesi
34	51	33.8	1091	1 IJCHNL	neural cell adhesi
35	51	33.8	1115	1 IJMSNL	neural cell adhesi
36	49	32.5	877	2 JX0256	DNA-directed DNA p
37	48.5	32.1	89	2 H69774	conserved hypothet
38	48.5	32.1	359	2 C84983	hypothetical prote
39	48.5	32.1	1765	2 A31494	DNA-directed RNA p
40	48.5	32.1	1765	2 B31494	DNA-directed RNA p
41	48.5	32.1	1766	2 B31875	DNA-directed RNA p
42	48.5	32.1	1766	2 A31875	DNA-directed RNA p
43	48	31.8	183	2 G69414	GMP synthase (guaa
44	48	31.8	369	2 JW0053	extracellular sign
45	47.5	31.5	619	2 S40938	hypothetical prote

ALIGNMENTS

RESULT 1
S43376
calreticulin, brain isoform 1 - bovine
C:Species: Bos primigenius taurus (cattle)
C:Date: 20-Oct-1994 #sequence_revision 23-Mar-1995 #text_change 07-May-1999
C:Accession: S43376; S36801
R:Matsuoka, K.; Seta, K.; Yamakawa, Y.; Okuyama, T.; Shinoda, T.; Isobe, T.
Biochem. J. 298, 435-442, 1994
A:Title: Covalent structure of bovine brain calreticulin.
A:Reference number: S43376; MUID:94183174
A:Accession: S43376
A:Molecule type: protein
A:Residues: 1-400 <MAT>
A:Experimental source: brain
R:Liu, N.; Fine, R.E.; Johnson, R.J.
Biochim. Biophys. Acta 1202, 70-76, 1993
A:Title: Comparison of cDNAs from bovine brain coding for two isoforms of calreticuli
A:Reference number: S36799; MUID:93385184
A:Accession: S36801
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 45-63, 'E', 65-83 <LIU>
A:Experimental source: brain, clone 8.1
C:Superfamily: calreticulin
C:Keywords: calcium binding; glycoprotein
F:397-400/Region: endoplasmic reticulum retention signal
F:120-146/Disulfide bonds: #status experimental
F:162/Binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match 100.0%; Score 151; DB 2; Length 400;
Best Local Similarity 100.0%; Pred. No. 3.5e-14;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGPGTKKHVIFNYKGNVLINKDIRC 27
Db 120 CGPGTKKHVIFNYKGNVLINKDIRC 146

RESULT 2
S06763
calreticulin precursor - mouse
N:Alternate names: 55K calcium-binding reticuloplasmin; calregulin
C:Species: Mus musculus (house mouse)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C:Accession: S06763; JCI444; PCI233; A57498
R:Smith, M.J.; Koch, G.L.E.
EMBO J. 8, 3581-3586, 1989
A:Title: Multiple zones in the sequence of calreticulin (CRP55, calregulin, HACBP), a
A:Reference number: S06763; MUID:90059955
A:Accession: S06763
A:Molecule type: DNA

A:Residues: 1-416 <SMI>
A:Cross-references: EMBL:X14926; NID:g50567; PIDN:CAA33053.1; PID:g50568
R:Marzartella, B.A.; Gold, P.; Cunningham, M.; Green, M.
Gene 120, 217-225, 1992
A:Title: Determination of the sequence of an expressible cDNA clone encoding Erp60/calreticulin
A:Reference number: JCI1444; MUID:93013037
A:Accession: JCI1444
A:Molecule type: mRNA
A:Residues: 1-416 <MAZ>
A:Cross-references: GB:M92988; NID:gl93084; PIDN:AAA37569.1; PID:gl93085
A:Accession: PC1233
A:Molecule type: protein
A:Residues: 18-41 <MAZ>
R:White, T.K.; Zhu, Q.; Tanzer, M.L.
J. Biol. Chem. 270, 15926-15929, 1995
A:Title: Cell surface calreticulin is a putative mannoside lectin which triggers mouse m...
A:Reference number: A57498; MUID:95332280
A:Accession: A57498
A>Status: Preliminary
A:Molecule type: protein
A:Residues: 74-80:142-151:186-193 <WHI>
C:Superfamily: calreticulin
C:Keywords: calcium binding
F:1-17/Domain: signal sequence #status predicted <SIG>
F:18-416/Product: calregulin #status experimental <MAT>
F:413-416/Region: endoplasmic reticulum retention signal

Query Match 100.0%; Score 151; DB 1; Length 416;
Best Local Similarity 100.0%; Pred. No. 3.6e-14;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGPGTKKVVHVIENYKGNVLINKDIRC 27
|||||
DB 137 CGPGTKKVVHVIENYKGNVLINKDIRC 163

RESULT 3
JH0819
calreticulin precursor - rat
N:Alternate names: calcium-binding protein 3
C:Species: Rattus norvegicus (Norway rat)
C:Date: 30-Sep-1993 #sequence_revision 20-Aug-1994 #text_change 20-Jun-2000
C:Accession: JH0819; A49176; S11205; PC1109; S45036; S04867; S39372; A34473; S13045
R:Nakamura, M.; Moriye, M.; Baba, T.; Michikawa, Y.; Yamanobe, T.; Arai, K.; Okinaga, S.
Exp. Cell Res. 205, 101-110, 1993
A:Title: An endoplasmic reticulum protein, calreticulin, is transported into the acrosom...
A:Reference number: A49176; MUID:93202172
A:Accession: JH0819
A:Molecule type: mRNA
A:Residues: 1-416 <NAK>
A:Cross-references: GB:D78308; NID:gl089798; PIDN:BA11345.1; PID:g1845572
A:Accession: A49176
A>Status: Preliminary
A:Molecule type: protein
A:Residues: 1-416 <NAZ>
A:Cross-references: GB:D78308; NID:gl089798; PIDN:BA11345.1; PID:g1845572
A:Experimental source: Sprague-Dawley, spermatogenic cells
A>Note: sequence extracted from NCHI backbone (NCBI:127639, NCBI:127643)
R:Murthy, K.K.; Banville, D.; Strikant, C.B.; Carrier, F.; Holmes, C.; Bell, A.; Patel, Y.
Nucleic Acids Res. 18, 4933, 1990
A:Title: Structural homology between the rat calreticulin gene product and the Onchocerc...
A:Reference number: S11205; MUID:90370496
A:Accession: S11205
A:Molecule type: mRNA
A:Residues: 1-416 <MUR>
A:Cross-references: EMBL:X53363; NID:g55854; PIDN:CAA37446.1; PID:g55855
R:Nakamura, M.; Michikawa, Y.; Baba, T.; Okinaga, S.; Arai, K.
Biochem. Biophys. Res. Commun. 186, 668-673, 1992
A:Title: Calreticulin is present in the acrosome of spermatids of rat testis.
A:Reference number: PC1109; MUID:92360010
A:Accession: PC1109
A:Molecule type: protein

A:Residues: 18-32 <NAK2>
A:Experimental source: testis, strain Sprague-Dawley
R:Soennichsen, B.; Fuellekrug, J.; van Nguyen, P.; Diekmann, W.; Robinson, D.G.; Mies
submitted to the EMBL Data Library, May 1994
A:Description: Retention and retrieval: both mechanisms cooperate to maintain calret...
A:Reference number: S45036
A:Accession: S45036
A>Status: Preliminary
A:Molecule type: mRNA
A:Residues: 1-416 <SOB>
A:Cross-references: EMBL:X79327; NID:g488840; PIDN:CAA55890.1; PID:g488841
R:Lone, Y.C.; Bailly, A.; Latruffe, N.
submitted to the EMBL Data Library, December 1988
A:Reference number: S04867
A:Accession: S04867
A:Molecule type: mRNA
A:Residues: 'R', 270-358, 'AAG' <LON>
A:Cross-references: EMBL:X13702; NID:g56055; PIDN:CAA31987.1; PID:g930260
A>Note: the authors designated the protein as D-beta-hydroxybutyrate dehydrogenase
R:Yokoi, T.; Nagayama, S.; Kajiwara, R.; Kawaguchi, Y.; Horiuchi, R.; Kanataki, T.
Biochim. Biophys. Acta 1158, 339-344, 1993
A:Title: Identification of protein disulfide isomerase and calreticulin as autoimmu...
A:Reference number: S39371; MUID:94072621
A:Accession: S39372
A:Molecule type: protein
A:Residues: 18-23, 'X', 25-32 <YOK>
R:Van, P.N.; Peter, F.; Soelling, H.D.
J. Biol. Chem. 264, 17494-17501, 1989
A:Title: Four intracisternal calcium-binding glycoproteins from rat liver microsomes
itive calcium sequestering rat liver vesicles.
A:Reference number: A34473; MUID:90008920
A:Accession: A34473
A>Status: Preliminary
A:Molecule type: protein
A:Residues: 18-36 <VAN>
R:Troves, S.; de Mattei, M.; Lanfredi, M.; Villa, A.; Green, N.M.; MacLennan, D.H.; M
Biochem. J. 271, 473-480, 1990
A:Title: Calreticulin is a candidate for a calsequestrin-like function in Ca(2+)-stor...
A:Reference number: S13045; MUID:91054414
A:Accession: S13045
A:Molecule type: protein
A:Residues: 18-29 <TRE>
C:Superfamily: calreticulin
C:Keywords: calcium binding; glycoprotein
F:1-17/Domain: signal sequence #status predicted <SIG>
F:18-416/Product: calreticulin #status experimental <MAT>
F:204-212/Region: nuclear location signal
F:413-416/Region: endoplasmic reticulum retention signal
F:344/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 100.0%; Score 151; DB 2; Length 416;
Best Local Similarity 100.0%; Pred. No. 3.6e-14;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGPGTKKVVHVIENYKGNVLINKDIRC 27
|||||
DB 137 CGPGTKKVVHVIENYKGNVLINKDIRC 163

RESULT 4
A37047
calreticulin precursor - human
N:Alternate names: 52K ribonucleoprotein autoantigen Ro/SS-A; 60K integrin-binding pr...
C:Species: Homo sapiens (man)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 18-Feb-2000
C:Accession: A42330; A37047; A46452; A28812; PH1525; A40346; S11475; T45075
R:McCaulliffe, D.P.; Yang, Y.S.; Wilson, J.; Sontheimer, R.D.; Capra, J.D.
J. Biol. Chem. 267, 2557-2562, 1992
A:Title: The 5'-flanking region of the human calreticulin gene shares homology with t...
A:Reference number: A42330; MUID:92129342
A:Accession: A42330
A:Molecule type: DNA

A:Residues: 1-417 <MC2>
A:Note: sequence extracted from NCBI backbone (NCBIN:78537, NCBIP:78536)
R:McCaulliffe, D.P.; Lux, F.A.; Lieu, T.S.; Sanz, I.; Hanke, J.; Newkirk, M.M.; Bachinski
J. Clin. Invest. 85, 1379-1391, 1990
A:Title: Molecular cloning, expression, and chromosome 19 localization of a human Ro/SS-
A:Reference number: A37047; MUID:90237213
A:Accession: A37047
A:Molecule type: mRNA
A:Residues: 1-417 <MC2>
A:CROSS-references: GB:M32294; NID:g337486; PIDN:AAA36582.1; PID:g337487
A:Note: the authors translated the codon CTA for residue 349 as Tyr
R:Roakech, L.A.; Haseib, J.A.; Meilof, J.F.; Smeenk, R.J.; Unnasch, T.R.; Greene, B.M.;
J. Immunol. 147, 3031-3039, 1991
A:Title: Characterization of the autoantigen calreticulin.
A:Reference number: A46452; MUID:92013129
A:Accession: A46452
A:Molecule type: mRNA
A:Residues: 1-417 <ROK>
A:CROSS-references: GB:M84739; NID:gl79881; PIDN:AAA51916.1; PID:gl79882
A:Note: sequence extracted from NCBI backbone (NCBIN:60749, NCBIP:60750)
R:Lieu, T.S.; Newkirk, M.M.; Capra, J.D.; Sontheimer, R.D.
J. Clin. Invest. 82, 96-101, 1988
A:Title: Molecular characterization of human Ro/SS-A antigen. Amino terminal sequence of
A:Reference number: A28812; MUID:88273610
A:Accession: A28812
A:Molecule type: protein
A:Residues: 18-41 <LIE>
A:Note: 18-Ala was also found
R:Dupuis, M.; Schaefer, E.; Krause, K.H.; Tschopp, J.
J. Exp. Med. 177, 1-7, 1993
A:Title: The calcium-binding protein calreticulin is a major constituent of lytic granul
A:Reference number: PH1525; MUID:93115648
A:Accession: PH1525
A:Molecule type: protein
A:Residues: 18-27 <DUP>
A:Experimental source: LAK cell
R:Roiani, M.V.; Finlay, B.B.; Gray, V.; Dedhar, S.
Biochemistry 30, 9859-9866, 1991
A:Title: In vitro interaction of a polypeptide homologous to human Ro/SS-A antigen (calr
A:Reference number: A40346; MUID:92002034
A:Accession: A40346
A:Molecule type: protein
A:Residues: 18-34, 'R' <ROU>
R:Krause, K.H.; Simmerman, H.K.B.; Jones, L.R.; Campbell, K.P.
Biochem. J. 270, 545-548, 1990
A:Title: Sequence similarity of calreticulin with a Ca(2+)-binding protein that co-purif
A:Reference number: S11475; MUID:90380058
A:Accession: S11475
A:Molecule type: protein
R:Lamerdin, J.; McCready, P.; Stilwagen, S.; Ramirez, M.; Carrano, A.
submitted to the EMBL Data Library, November 1996
A:Description: Characterization by genomic sequence analysis of a gene-rich 111 kb regio
A:Reference number: Z22906
A:Accession: T45075
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-417 <LAW>
A:CROSS-references: EMBL:AD000092; PIDN:AA851176.1
A:Experimental source: cell line 5HL2-B; fibroblast
C:Comment: Autoantibodies specific for this protein are found in Sjogren's syndrome and
C:Genetics:
A:Gene: GDB:CALR
A:CROSS-references: GDB:125179; OMIM:109091
A:Map position: 19p13.3-19p13.2
A:introns: 31/1; 65/1; 133/1; 164/3; 234/3; 272/3; 320/3; 351/3
A:Note: CRTG
C:Superfamily: calreticulin
C:Keywords: calcium binding; integrin binding
F:1-17/Domain: signal sequence #status predicted <SIG>
F:18-417/Product: calreticulin #status predicted <MAT>
F:414-417/Region: endoplasmic reticulum retention signal

Query Match 100.0%; Score 151; DB 1; Length 417;
Best Local Similarity 100.0%; Pred. No. 3.6e-14;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGPGTKKHVHFIYKGNVLINKDIRC 27
|||||
DB 137 CGPGTKKHVHFIYKGNVLINKDIRC 163

RESULT 5

A34154
calreticulin precursor, skeletal muscle - rabbit
C:Species: Oryctolagus cuniculus (domestic rabbit)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C:Accession: A34154; S13047
R:Fliegel, L.; Burns, K.; MacLennan, D.H.; Reithmeier, R.A.F.; Michalak, M.
J. Biol. Chem. 264, 21522-21528, 1989
A:Title: Molecular cloning of the high affinity calcium-binding protein (calreticulin
A:Reference number: A34154; MUID:90094320
A:Accession: A34154
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-418 <FLI>
A:CROSS-references: GB:J05138; NID:gl64858; PIDN:AAA31188.1; PID:gl64859
R:Treves, S.; de Mattei, M.; Lanfredi, M.; Villa, A.; Green, N.M.; MacLennan, D.H.; M
Biochem. J. 271, 473-480, 1990
A:Title: Calreticulin is a candidate for a calsequestrin-like function in Ca(2+)-stor
A:Reference number: S13045; MUID:91054414
A:Accession: S13047
A:Molecule type: protein
A:Residues: 19-32 <TRE>
C:Superfamily: calreticulin
C:Keywords: skeletal muscle
F:1-17/Domain: signal sequence #status predicted <SIG>
F:415-418/Region: endoplasmic reticulum retention signal

Query Match 100.0%; Score 151; DB 1; Length 418;
Best Local Similarity 100.0%; Pred. No. 3.6e-14;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGPGTKKHVHFIYKGNVLINKDIRC 27
|||||
DB 137 CGPGTKKHVHFIYKGNVLINKDIRC 163

RESULT 6

S36799
calreticulin precursor, brain isoform 2 - bovine
C:Species: Bos primigenius taurus (cattle)
C:Date: 10-Dec-1993 #sequence_revision 23-Mar-1995 #text_change 13-Aug-1999
C:Accession: S36799; S36800
R:Liu, N.; Fine, R.E.; Johnson, R.J.
Biochim. Biophys. Acta 1202, 70-76, 1993
A:Title: Comparison of cDNAs from bovine brain coding for two isoforms of calreticuli
A:Reference number: S36799; MUID:93385184
A:Accession: S36799
A:Molecule type: mRNA
A:Residues: 1-421 <LIU>
A:CROSS-references: GB:LI3462; NID:G348693; PIDN:AAC37307.1; PID:G348694
A:Experimental source: brain, clone 9.4
A:Accession: S36800
A:Molecule type: protein
A:Residues: 35-45 <LI2>
C:Superfamily: calreticulin
C:Keywords: calcium binding; glycoprotein
F:1-34/Domain: signal sequence #status predicted <SIG>
F:35-421/Product: calreticulin, brain isoform 2 #status predicted <MAT>
F:418-421/Region: endoplasmic reticulum retention signal
F:141-167/Disulfide bonds: #status predicted
F:183/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 100.0%; Score 151; DB 2; Length 421;
 Best Local Similarity 100.0%; Pred. No. 3, 7e-14;
 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGPGTKKHVHVFYKGNVLIINKDIRC 27
 |||||
 DB 141 CGPGTKKHVHVFYKGNVLIINKDIRC 167

RESULT 7
 JH0795
 calreticulin precursor - California sea hare
 N:Alternative names: protein 407
 C:Species: Aplysia californica (California sea hare)
 C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
 C:Accession: JH0795; B31409; F60977
 R:Kennedy, T.E.; Kuhl, D.; Barzilai, A.; Sweatt, J.D.; Kandel, E.R.
 Neuron 9, 1013-1024, 1992
 A:Title: Long-term sensitization training in aplysia leads to an increase in calreticulin
 A:Reference number: JH0795; MUID:93098937
 A:Accession: JH0795
 A:Molecule type: mRNA
 A:Residues: 1-405 <K>
 A:Cross-references: GB:S51239; MID:q262053; PIDN:AA824569.1; PID:q262054
 A:Experimental source: abdominal ganglion and antral nervous system
 R:Kennedy, T.E.; Gawinowicz, M.A.; Barzilai, A.; Kandel, E.R.; Sweatt, J.D.
 Proc. Natl. Acad. Sci. U.S.A. 85, 7008-7012, 1988
 A:Title: Sequencing of proteins from two-dimensional gels by using in situ digestion and
 tion in Aplysia.
 A:Reference number: A94207; MUID:88320566
 A:Accession: B31409
 A:Molecule type: protein
 A:Residues: 'X', 17-28, 'X', 30-31 <K>
 R:Sweatt, J.D.; Kennedy, T.E.; Wager-Smith, K.; Gawinowicz, M.A.; Barzilai, A.; Karl, K.
 Electrophoresis 10, 152-157, 1989
 A:Title: Development of a database of amino acid sequences for proteins identified and
 A:Reference number: A60977; MUID:89276264
 A:Accession: F60977
 A:Molecule type: protein
 A:Residues: 'X', 17-28, 'X', 30-31 <SW>
 C:Superfamily: calreticulin
 C:Keywords: calcium binding; endoplasmic reticulum
 F:1-15/Domain: signal sequence #status predicted <SIG>
 F:16-405/Product: calreticulin #status experimental <MAT>
 F:402-405/Region: endoplasmic reticulum retention signal

Query Match 93.4%; Score 141; DB 1; Length 405;
 Best Local Similarity 88.9%; Pred. No. 9, 9e-13;
 Matches 24; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 CGPGTKKHVHVFYKGNVLIINKDIRC 27
 |||||
 DB 133 CGPGTKKHVHVFYKGNVLIINKDIRC 159

RESULT 8
 A36637
 calreticulin homolog precursor - fruit fly (Drosophila melanogaster)
 N:Alternative names: Ro/SS-A autoantigen/calreticulin homolog
 C:Species: Drosophila melanogaster
 C:Date: 11-Aug-1995 #sequence_revision 11-Aug-1995 #text_change 13-Aug-1999
 C:Accession: A56637; A37158
 R:Smith, M.J.
 DNA Seq. 3, 247-250, 1992
 A:Title: Nucleotide sequence of a Drosophila melanogaster gene encoding a calreticulin h
 A:Reference number: A56637; MUID:93208374
 A:Accession: A56637
 A:Status: Preliminary
 A:Molecule type: DNA
 A:Residues: 1-406 <SM>
 A:Cross-references: GB:X64461; MID:g7685; PIDN:CAA45791.1; PID:g7686

A:Note: sequence extracted from NCBI backbone (NCBIN:128274, NCBIP:128275)
 R:McCaulliffe, D.P.; Zappi, E.; Lileu, T.S.; Michalak, M.; Sontheimer, R.D.; Capra, J.D
 J. Clin. Invest. 86, 332-335, 1990
 A:Title: A human Ro/SS-A autoantigen is the homologue of calreticulin and is highly h
 A:Reference number: A37158; MUID:90307981
 A:Accession: A37158
 A:Status: Preliminary; nucleic acid sequence not shown; not compared with conceptual
 A:Molecule type: DNA
 A:Residues: 91-105, 'A', 107, 109-124; 182-183, 'L', 185-220 <MCC>
 C:Genetics:
 A:Gene: FlyBase:Crc
 A:Cross-references: FlyBase:FBgn0005585
 A:Introns: 65/1; 222/3
 C:Superfamily: calreticulin
 C:Keywords: calcium binding; endoplasmic reticulum
 F:1-17/Domain: signal sequence #status predicted <SIG>
 F:403-406/Region: endoplasmic reticulum retention signal

Query Match 88.7%; Score 134; DB 2; Length 406;
 Best Local Similarity 88.9%; Pred. No. 1e-11;
 Matches 24; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 CGPGTKKHVHVFYKGNVLIINKDIRC 27
 |||||
 DB 137 CGPGTKKHVHVFYKGNVLIINKDIRC 163

RESULT 9
 S71343
 calreticulin precursor - Korean frog
 C:Species: Rana rugosa (Korean frog)
 C:Date: 29-Jan-1998 #sequence_revision 13-Feb-1998 #text_change 20-Jun-2000
 C:Accession: S71343
 R:Yamamoto, S.; Nakamura, M.
 FEBS Lett. 387, 27-32, 1996
 A:Title: Calnexin: its molecular cloning and expression in the liver of the frog, Ran
 A:Reference number: S71342; MUID:96234004
 A:Accession: S71343
 A:Status: nucleic acid sequence not shown
 A:Molecule type: mRNA
 A:Residues: 1-419 <Y>
 A:Cross-references: EMBL:D78589; MID:g1514956; PIDN:BAAL1425.1; PID:g1514957
 C:Superfamily: calreticulin
 C:Keywords: calcium binding; endoplasmic reticulum
 F:1-18/Domain: signal sequence #status predicted <SIG>
 F:19-419/Product: calreticulin #status predicted <MAT>
 F:205-213/Region: nuclear location signal
 F:415-418/Region: endoplasmic reticulum retention signal

Query Match 82.8%; Score 125; DB 2; Length 419;
 Best Local Similarity 88.5%; Pred. No. 2.1e-10;
 Matches 23; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 CGPGTKKHVHVFYKGNVLIINKDIRC 26
 |||||
 DB 138 CGPGTKKHVHVFYKGNVLIINKDIRC 163

RESULT 10
 A32507
 41k larval antigen - nematode (Onchocerca volvulus) (fragment)
 C:Species: Onchocerca volvulus
 C:Date: 21-May-1990 #sequence_revision 21-May-1990 #text_change 12-Apr-1995
 C:Accession: A32507; A28813
 R:Unnasch, T.R.; Gallin, M.V.; Soboslay, P.T.; Erttmann, K.D.; Greene, B.M.
 J. Clin. Invest. 82, 262-269, 1988
 A:Title: Isolation and characterization of expression cDNA clones encoding antigens o
 A:Reference number: A92769; MUID:88273584
 A:Accession: A32507
 A:Molecule type: mRNA
 A:Residues: 1-336 <UN>

C:Superfamily: calreticulin

Query Match 80.1%; Score 121; DB 2; Length 336;
Best Local Similarity 77.8%; Pred. No. 6.5e-10;
Matches 21; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 CGPGTKKHVIFNYKGNVLINKDIRC 27
|||||
DB 83 CGPGTKKHVIFNYKGNVLINKDIRC 109

RESULT 11

S29130
calreticulin (clone 8) - African clawed frog (fragment)
C:Species: Xenopus laevis (African clawed frog)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 13-Aug-1999
C:Accession: S29130; T01068
R:Trevies, S.; Zorzato, F.; Pozzan, T.
Biochem. J. 287, 579-581, 1992
A:Title: Identification of calreticulin isoforms in the central nervous system.
A:Reference number: S29129; MUID:93074997
C:Accession: S29130
A:Molecule type: mRNA
A:Residues: 1-384 <TRE>
A:Cross-references: EMBL:X67598
A:Accession: T01068
A:Status: translated from GB/EMBL/DBDJ
A:Molecule type: mRNA
A:Residues: 1-339, 'XTGR' <TRW>
A:Cross-references: EMBL:X67598; NID:964610; PIDN:CAA47867.1; PID:964611
A:Experimental source: CNS
C:Superfamily: calreticulin
C:Keywords: glycoprotein
F:381-384/Region: endoplasmic reticulum retention signal
F:316/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 79.5%; Score 120; DB 2; Length 384;
Best Local Similarity 81.5%; Pred. No. 1e-09;
Matches 22; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 CGPGTKKHVIFNYKGNVLINKDIRC 27
|||||
DB 109 CGPGTKKHVIFNYKGNVLINKDIRC 135

RESULT 12

S29129
calreticulin precursor (clone 3) - African clawed frog (fragment)
C:Species: Xenopus laevis (African clawed frog)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 13-Aug-1999
C:Accession: S29129
R:Trevies, S.; Zorzato, F.; Pozzan, T.
Biochem. J. 287, 579-581, 1992
A:Title: Identification of calreticulin isoforms in the central nervous system.
A:Reference number: S29129; MUID:93074997
C:Accession: S29129
A:Molecule type: mRNA
A:Residues: 1-411 <TRE>
A:Cross-references: EMBL:X67597; NID:964608; PIDN:CAA47866.1; PID:964609
C:Superfamily: calreticulin
C:Keywords: glycoprotein
F:1-12/Domain: signal sequence (fragment) #status predicted <SIG>
F:13-411/Product: calreticulin #status predicted <MAT>
F:408-411/Region: endoplasmic reticulum retention signal
F:339/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 79.5%; Score 120; DB 2; Length 411;
Best Local Similarity 81.5%; Pred. No. 1.1e-09;
Matches 22; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 CGPGTKKHVIFNYKGNVLINKDIRC 27
|||||
DB 132 CGPGTKKHVIFNYKGNVLINKDIRC 158

RESULT 13

A48573
calreticulin autoantigen homolog precursor - fluke (Schistosoma mansoni)
C:Species: Schistosoma mansoni
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C:Accession: A48573
R:Khalife, J.; Trottein, F.; Schacht, A.M.; Godin, C.; Pierce, R.J.; Capron, A.
Mol. Biochem. Parasitol. 57, 193-202, 1993
A:Title: Cloning of the gene encoding a Schistosoma mansoni antigen homologous to hum
A:Reference number: A48573; MUID:93165070
C:Accession: A48573
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-393 <KHA>
A:Cross-references: GB:M93097; NID:gl60928
A:Note: sequence inconsistent with the nucleotide translation
A:Note: sequence extracted from NCBI backbone (NCBIN:125085, NCBIP:125086)
C:Superfamily: calreticulin
F:1-16/Domain: signal sequence
F:390-393/Region: endoplasmic reticulum retention signal

Query Match 74.2%; Score 112; DB 1; Length 393;
Best Local Similarity 77.8%; Pred. No. 1.5e-08;
Matches 21; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 CGPGTKKHVIFNYKGNVLINKDIRC 27
|||||
DB 135 CGMATKKHVIFNYKGNHLIKKEIPC 161

RESULT 14

S25851
calreticulin precursor - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 06-Jan-1994 #sequence_revision 10-Nov-1995 #text_change 05-Nov-1999
C:Accession: S25851; T33996
R:Smith, M.J.
DNA Seq. 2, 235-240, 1992
A:Title: A C. elegans gene encodes a protein homologous to mammalian calreticulin.
A:Reference number: S25851; MUID:92329978
C:Accession: S25851
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-395 <SMI>
A:Cross-references: EMBL:X59589; NID:g6693; PIDN:CAA42159.1; PID:g6694
R:Bauer, C.; Courtney, L.; Laplant, Y.
submitted to the EMBL Data Library, February 1999
A:Description: The sequence of C. elegans cosmid Y38A10A.
A:Reference number: Z21453
C:Accession: T33996
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: DNA
A:Residues: 1-395 <BAU>
A:Cross-references: EMBL:AF125963; PIDN:AAD14746.1; GSPDB:GN00023; CESP:Y38A10A.5
A:Experimental source: strain Bristol N2; clone Y38A10A
C:Genetics:
A:Gene: CESP:Y38A10A.5
A:Map position: 5
A:Introns: 107/3; 315/3
C:Superfamily: calreticulin
F:1-15/Domain: signal sequence #status predicted <SIG>
F:392-395/Region: endoplasmic reticulum retention signal

Query Match 63.9%; Score 96.5; DB 2; Length 395;
Best Local Similarity 66.7%; Pred. No. 2.7e-06;
Matches 18; Conservative 4; Mismatches 4; Indels 1; Gaps 1;

QY 1 CGPCTKKVHVNIYKGNVLIINKDIRC 27
DB 133 CGP-TRRVHVLINIKGNLIINKKEITC 158
RESULT 15
T14554
calreticulin - beet
C:Species: Beta vulgaris (beet)
C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Jun-2000
C:Accession: T14554
R:Viereck, R.
submitted to the EMBL Data Library, October 1997
A:Description: Nucleotide sequence from sugar beet calreticulin.
A:Reference number: Z18137
A:Accession: T14554
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: mRNA
A:Residues: 1-416 <VIE>
A:Cross-references: EMBL:AJ020257
A:Experimental source: strain diploide Inzuchtlinie KWS; leaf
C:Superfamily: calreticulin
C:Keywords: calcium binding

Query Match 60.9%; Score 92; DB 2; Length 416;
Best Local Similarity 63.0%; Pred. No. 1.3e-05;
Matches 17; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

QY 1 CGPCTKKVHVNIYKGNVLIINKDIRC 27
DB 143 CGYSTKKVHAIFNIYNDTNHLIKKDVPC 169

Search completed: January 9, 2002, 15:02:03
Job time: 190 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: January 9, 2002, 15:12:14 ; Search time 25.18 Seconds
(without alignments)
88.823 Million cell updates/sec

Title: US-09-828-000-4
Perfect score: 340
Sequence: 1 TDMHGDSEYNMFPGDICGP.....IRCKDDEFTHTLVIRPDN 61

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 100059 seqs, 36664827 residues

Total number of hits satisfying chosen parameters: 100059

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_39:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query %	Match	Length	DB ID	Description
1	340	100.0	417	1	CRTC_HUMAN	P27797 homo sapien
2	335	98.5	400	1	CRTL_BOVIN	P52193 bos taurus
3	335	98.5	416	1	CRTC_MOUSE	P14211 mus musculus
4	335	98.5	416	1	CRTC_RAT	P18418 rattus norv
5	335	98.5	418	1	CRTC_RABIT	P15253 oryctolagus
6	335	98.5	421	1	CRTL_BOVIN	P42918 bos taurus
7	293	86.2	406	1	CRTC_DROME	P29413 drosophila
8	261	76.8	388	1	RALL_ONCVO	P11012 onchocerca
9	242	71.2	393	1	CRTC_SCHMA	Q06814 schistosoma
10	233.5	68.7	395	1	CRTC_CAEL	P27798 caenorhabdi
11	220	64.7	420	1	CRTC_CHLRE	Q9std3 chlamydomon
12	207	60.9	416	1	CRTC_BETVU	O81919 beta vulgar
13	204	60.0	421	1	CRTC_PRUAR	Q9xf98 prunus arme
14	202	59.4	415	1	CRTC_RICCO	P93508 ricinus com
15	202	59.4	424	1	CRTL_ARATH	Q38858 arabidopsis
16	199	58.5	425	1	CRTL_ARATH	O04151 arabidopsis
17	195	57.4	424	1	CRTC_DICDI	O23858 dictyosteli
18	195	57.4	424	1	CRTC_ORVSA	O9slv8 oryza sativ
19	194	57.1	424	1	CRTL_ARATH	O04153 arabidopsis
20	191	56.2	416	1	CRTC_NICPL	Q40401 nicotiana p
21	183	53.8	416	1	CRTC_BERST	Q9zpp1 berberis st
22	177.5	52.2	401	1	CRTC_EUGGR	Q92ny3 euglena gra
23	163	47.9	420	1	CRTC_MAIZE	O9sp22 zea mays (m
24	122.5	36.0	546	1	CALX_SOYEN	Q39817 glycine max
25	121.5	35.7	592	1	CALX_HUMAN	P27824 homo sapien
26	120.5	35.4	591	1	CALX_MOUSE	P35564 mus musculus
27	120.5	35.4	591	1	CALX_RAT	P35565 rattus norv
28	120.5	35.4	593	1	CALX_CANFA	P24643 canis fami
29	115.5	34.0	530	1	CALX_ARATH	P29402 arabidopsis
30	115.5	34.0	540	1	CALX_HELTU	Q39994 helianthus
31	115.5	34.0	619	1	CALX_CAEL	P34652 caenorhabdi
32	112.5	33.1	551	1	CALX_PEA	O82709 pisum sativ
33	108.5	31.9	611	1	CALG_MOUSE	P52194 mus musculus

RESULT 1

ID	CRTC_HUMAN	STANDARD:	PRT:	417 AA.
AC	P27797;			
DT	01-AUG-1992 (Rel. 23, Created)			
DT	01-AUG-1992 (Rel. 23, Last sequence update)			
DT	20-AUG-2001 (Rel. 40, Last annotation update)			
DE	CALRETICULIN PRECURSOR (CRP55) (CALREGULIN) (HACBP) (ERP60) (52 KDA			
DE	RIBONUCLEOPROTEIN AUTOANTIGEN RO/SS-A).			
GN	CALR OR CRTC.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=92013129; PubMed=1919005;			
RA	Rokeach L.A., Haselby J.A., Mellof J.F., Smeenk R.J., Unnasch T.R.,			
RA	Greene B.M., Hoch S.O.;			
RT	"Characterization of the autoantigen calreticulin.";			
RL	J. Immunol. 147:3031-3039(1991).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=90237213; PubMed=2332496;			
RA	McCaulliffe D.P., Lux F.A., Lieu T.S., Sanz I., Hanke J., Newkirk M.M.,			
RA	Bachinski L.L., Itoh Y., Siciliano M.J., Reichlin M., Sontheimer R.D.,			
RA	Capra J.D.;			
RT	"Molecular cloning, expression, and chromosome 19 localization of a			
RT	human Ro/SS-A autoantigen.";			
RL	J. Clin. Invest. 85:1379-1391(1990).			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=92129342; PubMed=1733953;			
RA	McCaulliffe D.P., Yang Y.S., Willson J., Sontheimer R.D., Capra J.D.;			
RT	"The 5'-flanking region of the human calreticulin gene shares			
RT	homology with the human GRP78, GRP94, and protein disulfide isomerase			
RT	promoters.";			
RL	J. Biol. Chem. 267:2557-2562(1992).			
RN	[4]			
RP	SEQUENCE FROM N.A.			
RA	Lamerdin J., McCreedy P., Stilwagen S., Ramirez M., Carrano A.;			
RL	Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.			
RN	[5]			
RP	SEQUENCE OF 18-36.			
RX	MEDLINE=92002034; PubMed=1911778;			
RA	Rojiani M.V., Finlay B.B., Gray V., Dedhar S.;			
RT	"In vitro interaction of a polypeptide homologous to human Ro/SS-A			
RT	antigen (calreticulin) with a highly conserved amino acid sequence in			
RT	the cytoplasmic domain of integrin alpha subunits.";			
RL	Biochemistry 30:9859-9866(1991).			
RN	[6]			
RP	SEQUENCE OF 18-32.			
RX	MEDLINE=90380058; PubMed=2400400;			
RA	Krause K.H., Simmerman H.K.B., Jones L.R., Campbell K.P.;			
RT	"Sequence similarity of calreticulin with a Ca2(+)-binding protein			
RT	that co-purifies with an Ins(1,4,5)P3-sensitive Ca2+ store in HL-60			

ALIGNMENTS

34	105.5	31.0	528	1	CAX2_ARATH	Q38798 arabidopsis
35	103.5	30.4	610	1	CALG_HUMAN	O14967 homo sapien
36	103	30.3	560	1	CALX_SCHPO	P36581 schizosacch
37	77.5	22.8	540	1	MTAL_ACICA	P25201 actinetobact
38	66	19.4	560	1	YECO_YEAST	P39994 saccharomyc
39	64.5	19.0	1766	1	RPBL_TRYBB	P17545 trypanosoma
40	64.5	19.0	1766	1	RPB2_TRYBB	P17546 trypanosoma
41	63.5	18.7	489	1	YN98_YEAST	P53755 saccharomyc
42	63.5	18.7	502	1	CALX_YEAST	P27825 saccharomyc
43	59	17.4	1361	1	YME9_YEAST	O04693 saccharomyc
44	58	17.1	286	1	RIPL_MOMCH	P16094 momordica c
45	58	17.1	496	1	NUSA_BUCAI	P57459 buchnera ap

RT cells.";
 RL Biochem. J. 270:545-548(1990).
 [7]
 RN
 RP SKOURNCE OF 18-28.
 RC
 RX MEDLINE-93162045; PubMed 1286669;
 RA Hochstrasser D.F., Frutiger S., Paquet N., Bairoch A., Ravier F.,
 RA Pasquali C., Sanchez J.-C., Tissot J.-D., Bjellqvist B., Vargas R.,
 RA Appel R.D., Hughes G.J.;
 RT "Human liver protein map: a reference database established by
 RT microsequencing and gel comparison.";
 RT Electrophoresis 13:992-1001(1992).
 [8]
 RN
 RP PARTIAL SEQUENCE OF 25-34; 56-62; 208-221 AND 273-278.
 RC
 RX TISSUE-Keratinocytes;
 KX MEDLINE-93162043; PubMed 1286667;
 RA Rasmussen H.H., van Damme J., Puype M., Gesser B., Celis J.E.,
 RA Vandekerckhove J.;
 RT "Microsequences of 145 proteins recorded in the two-dimensional gel
 RT protein database of normal human epidermal keratinocytes.";
 RL Electrophoresis 13:960-969(1992).
 [9]
 RN
 RP SEQUENCE OF 18-26.
 RC
 RX TISSUE-Colon carcinoma;
 RX MEDLINE-97295306; PubMed-9150948;
 RA Ji H., Reid G.E., Moritz R.L., Eddes J.S., Burgess A.W., Simpson R.J.;
 RT "A two-dimensional gel database of human colon carcinoma proteins.";
 RL Electrophoresis 18:605-613(1997).
 CC
 CC -1- FUNCTION: THIS PROTEIN BINDS CALCIUM. THERE ARE BOTH HIGH AND
 CC LOW AFFINITY CALCIUM-BINDING SITES.
 CC
 CC -1- SUBUNIT: MONOMER (BY SIMILARITY).
 CC
 CC -1- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM LUMEN.
 CC
 CC -1- SIMILARITY: BELONGS TO THE CALRETICULIN FAMILY.
 CC
 CC -1- CAUTION: WAS ORIGINALLY (REF.2) THOUGHT TO BE THE RO AUTOANTIGEN.
 CC
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 CC
 CC EMBL; M84739; AAA51916.1; -;
 DR EMBL; M32294; AAA36582.1; -;
 DR EMBL; AD000092; AAB51176.1; -;
 DR PIR; A37047; A37047.
 DR PIR; S11475; S11475.
 DR PIR; A42330; A42330.
 DR PIR; A46452; A46452.
 DR SWISS-2DPAGE; P27797; HUMAN
 DR Ayrhus/Ghent-2DPAGE; 9401; IEF.
 DR HSC-2DPAGE; P27797; HUMAN.
 DR MIM; 109091; -;
 DR InterPro; IPR001580; Calreticulin.
 DR InterPro; IPR000886; ER_target.
 DR Pfam; PF00262; calreticulin; 1.
 DR PRINTS; PR00626; CALRETICULIN.
 DR PRODOM; PD001866; Calreticulin; 1.
 DR PROSITE; PS00014; ER_TARGET; 1.
 DR PROSITE; PS00803; CALRETICULIN_1; 1.
 DR PROSITE; PS00804; CALRETICULIN_2; 1.
 DR PROSITE; PS00805; CALRETICULIN_REPEAT; 3.
 KW Endoplasmic reticulum; Calcium-binding; Repeat; Signal.
 FT SIGNAL 1 17
 FT CHAIN 18 417 CALRETICULIN.
 FT DOMAIN 18 197 N-DOMAIN.
 FT DOMAIN 198 308 P-DOMAIN.
 FT DOMAIN 309 417 C-DOMAIN.
 FT DOMAIN 191 255 4 X APPROXIMATE REPEATS.
 FT REPEAT 191 202 1-1.
 FT REPEAT 210 221 1-2.
 FT REPEAT 227 238 1-3.

FT REPEAT 244 255 1-4.
 FT DOMAIN 259 297 3 X APPROXIMATE REPEATS.
 FT REPEAT 259 283 2-1.
 FT REPEAT 273 283 2-2.
 FT REPEAT 287 297 2-3.
 FT DOMAIN 351 408 ASP/GLU/LYS-RICH.
 FT DISULFID 137 163 BY SIMILARITY.
 FT SITE 414 417 PREVENT SECRETION FROM ER.
 FT CONFLICT 35 35 MISSING (IN REF. 3).
 SQ SEQUENCE 417 AA; 48141 MW; BC37C3C0F1054FB2 CRC64;
 Query Match 100.0%; Score 340; DB 1; Length 417;
 Best Local Similarity 100.0%; Pred. No. 3.4e-34; Indels 0; Gaps 0;
 Matches 61; Conservative 0; Mismatches 0;
 QY 1 TDMHGDSYNIAMFGPDICGPTGKVKHVIENYKGNVINKRDKDDETHLYTLVRPD 60
 Db 120 TDMHGDSYNIAMFGPDICGPTGKVKHVIENYKGNVINKRDKDDETHLYTLVRPD 179
 QY 61 N 61
 Db 180 N 180
 RESULT 2
 CRTI_BOVIN
 ID CRTI_BOVIN STANDARD; PRT; 400 AA.
 AC P52193;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 01-OCT-1996 (Rel. 34, Last annotation update)
 DE CALRETICULIN, BRAIN ISOFORM 1 (CRP55) (CALREGULIN) (HACBP).
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 OX NCBI_TaxID-9913;
 RN [1]
 RP SEQUENCE.
 RC TISSUE-Brain;
 RX MEDLINE-94183174; PubMed-8135753;
 RA Matsuoka K., Seta K., Yamakawa Y., Okuyama T., Shinoda T., Isobe T.;
 RT "Covalent structure of bovine brain calreticulin.";
 RL Biochem. J. 298:435-442(1994).
 CC
 CC -1- FUNCTION: THIS PROTEIN BINDS CALCIUM. THERE ARE BOTH HIGH AND
 CC LOW AFFINITY CALCIUM-BINDING SITES.
 CC
 CC -1- SUBUNIT: MONOMER.
 CC
 CC -1- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM LUMEN.
 CC
 CC -1- SIMILARITY: BELONGS TO THE CALRETICULIN FAMILY.
 DR InterPro; IPR001580; Calreticulin.
 DR InterPro; IPR000886; ER_target.
 DR Pfam; PF00262; calreticulin; 1.
 DR PRINTS; PR00626; CALRETICULIN.
 DR PRODOM; PD001866; Calreticulin; 1.
 DR PROSITE; PS00014; ER_TARGET; 1.
 DR PROSITE; PS00803; CALRETICULIN_1; 1.
 DR PROSITE; PS00804; CALRETICULIN_2; 1.
 DR PROSITE; PS00805; CALRETICULIN_REPEAT; 3.
 KW Endoplasmic reticulum; Calcium-binding; Repeat; Glycoprotein.
 FT DOMAIN 1 180 N-DOMAIN.
 FT DOMAIN 181 291 P-DOMAIN.
 FT DOMAIN 292 400 C-DOMAIN.
 FT DOMAIN 174 238 4 X APPROXIMATE REPEATS.
 FT REPEAT 174 185 1-1.
 FT REPEAT 193 204 1-2.
 FT REPEAT 210 221 1-3.
 FT REPEAT 227 238 1-4.
 FT DOMAIN 242 280 3 X APPROXIMATE REPEATS.
 FT REPEAT 242 252 2-1.
 FT REPEAT 256 266 2-2.
 FT REPEAT 270 280 2-3.
 FT DOMAIN 334 390 ASP/GLU/LYS-RICH.

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FT DISULFID 120 146
FT CARBOHYD 162 162
FT SITE 397 400
SQ SEQUENCE 400 AA: 46381 MW; 7D4B68DFC689EEF1 CRC64;

Query Match 98.5%; Score 335; DB 1; Length 400;
Best Local Similarity 98.4%; Pred. No. 1.3e-33;
Matches 60; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TMHGDSEYNIMFGPDICGPGTKKVVHVFYKGNVKNVINKDIRCKDDETHLYTLIVRPD 60
DB 103 TMHGDSEYNIMFGPDICGPGTKKVVHVFYKGNVKNVINKDIRCKDDETHLYTLIVRPN 162

QY 61 N 61
DB 163 N 163

RESULT 3
CRTC_MOUSE
ID CRTC_MOUSE STANDARD; PRT: 416 AA.
AC P14211;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE CALRETICULIN PRECURSOR (CRP55) (CALREGULIN) (HACBP) (ERP60).
GN CALR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 18-48 AND 129-161.
RC STRAIN=BALB/C; TISSUE=Liver;
RX MEDLINE=90059955; PubMed=2583110;
RA Smith M.J., Koch G.L.E.;
RT "Multiple zones in the sequence of calreticulin (CRP55, calregulin, HACBP), a major calcium binding ER/SR protein.";
RL EMBO J. 8:3581-3586(1989).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=93013037; PubMed=1398135;
RA Mazzarella R.A., Gold P., Cunningham M., Green M.;
RT "Determination of the sequence of an expressible cDNA clone encoding ERp60/calregulin by the use of a novel nested set method.";
RL Gene 120:217-225(1992).
RN [3]
RP SEQUENCE OF 18-38.
RC TISSUE=Fibroblast;
RX MEDLINE=95009907; PubMed=7523108;
RA Merrick B.A., Patterson R.M., Wichter L.L., He C., Selkirk J.K.;
RT "Separation and sequencing of familial and novel murine proteins using preparative two-dimensional gel electrophoresis.";
RL Electrophoresis 15:735-745(1994).
CC -!- FUNCTION: THIS PROTEIN BINDS CALCIUM. THERE ARE BOTH HIGH AND LOW AFFINITY CALCIUM-BINDING SITES.
CC -!- SUBUNIT: MONOMER (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM LUMEN.
CC -!- SIMILARITY: BELONGS TO THE CALRETICULIN FAMILY.
CC -----
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CC -----
DB EMBL; X14926; CAA33053.1; -
DR EMBL; M92988; AAA37569.1; -
DR PIR; S06763; S06763.
DR PIR; JC1444; JC1444.
```

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DR SWISS-2DPAGE; P14211; MOUSE.
MGD; MGI:88252; Calr.
DR InterPro; IPR001580; Calreticulin.
DR InterPro; IPR000886; ER_target.
DR Pfam; PF00262; calreticulin; 1.
DR PRINTS; PR00626; CALRETICULIN.
DR PRODOM; PD001866; Calreticulin; 1.
DR PROSITE; PS00014; ER_TARGET; 1.
DR PROSITE; PS00803; CALRETICULIN_1; 1.
DR PROSITE; PS00804; CALRETICULIN_2; 1.
DR PROSITE; PS00805; CALRETICULIN_REPEAT; 3.
KW Endoplasmic reticulum; Calcium-binding; Repeat; Signal.
FT SIGNAL 1 17
FT CHAIN 18 416 CALRETICULIN.
FT DOMAIN 18 197 N-DOMAIN.
FT DOMAIN 198 308 P-DOMAIN.
FT DOMAIN 309 416 C-DOMAIN.
FT DOMAIN 191 255 4 X APPROXIMATE REPEATS.
FT REPEAT 191 202 1-1.
FT REPEAT 210 221 1-2.
FT REPEAT 227 238 1-3.
FT REPEAT 244 255 1-4.
FT DOMAIN 259 297 3 X APPROXIMATE REPEATS.
FT REPEAT 259 269 2-1.
FT REPEAT 273 283 2-2.
FT REPEAT 287 297 2-3.
FT DOMAIN 351 407 ASP/GLU/LYS-RICH.
FT DISULFID 137 163 BY SIMILARITY.
FT SITE 413 416 PREVENT SECRETION FROM ER.
SQ SEQUENCE 416 AA: 47994 MW; 24C03B00913408D8 CRC64;

Query Match 98.5%; Score 335; DB 1; Length 416;
Best Local Similarity 100.08; Pred. No. 1.4e-33;
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DMHGDSEYNIMFGPDICGPGTKKVVHVFYKGNVKNVINKDIRCKDDETHLYTLIVRPD 61
DB 121 DMHGDSEYNIMFGPDICGPGTKKVVHVFYKGNVKNVINKDIRCKDDETHLYTLIVRPD 180

RESULT 4
CRTC_RAT
ID CRTC_RAT STANDARD; PRT: 416 AA.
AC P18418; P10452;
DT 01-MAR-1989 (Rel. 10, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE CALRETICULIN PRECURSOR (CRP55) (CALREGULIN) (HACBP) (ERP60) (CALBP) (CALR).
GN CALR.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SPRAGUE-DAWLEY; TISSUE=Brain cortex;
RX MEDLINE=90370496; PubMed=2395661;
RA Murthy K.K., Banville D., Srikanth C.B., Carrier F., Bell A., Holmes C., Patel Y.C.;
RT "Structural homology between the rat calreticulin gene product and the Onchocerca volvulus antigen Rat-1.";
RL Nucleic Acids Res. 18:4933-4933(1990).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=SPRAGUE-DAWLEY;
RX MEDLINE=93202172; PubMed=8453984;
RA Nakamura M., Moriya M., Baba T., Michikawa Y., Yamanobe T., Arai K., Okinaga S., Kobayashi T.;
RT "An endoplasmic reticulum protein, calreticulin, is transported into the acrosome of rat sperm.";
RL Exp. Cell Res. 205:101-110(1993).
```

[3]
 RP SEQUENCE FROM N.A.
 RC STRAIN SPRAGUE-DAWLEY; TISSUE: Liver;
 RX MEDLINE-95181573; PubMed-7876339;
 RA Sennichsen B., Fliedekrug J., van Nguyen P., Diekmann W.,
 RA Robinson D.G., Fieskes G.;
 RT "Retention and retrieval: both mechanisms cooperate to maintain
 RT calreticulin in the endoplasmic reticulum.";
 RL J. Cell Sci. 107:2705-2717(1994).
 [4]
 RP SEQUENCE OF 270-358 FROM N.A.
 RC STRAIN SPRAGUE-DAWLEY;
 KA Lone Y.C., Bailey A., Latruffe N.;
 RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
 [5]
 RP SEQUENCE OF 18-29.
 RX MEDLINE-91054414; PubMed-2241926;
 RA Treves S., de Mattei M., Lanfredi M., Villa A., Green N.M.,
 RA MacLennan D.H., Meldolesi J., Pozzan T.;
 RT "Calreticulin is a candidate for a calsequestrin-like function in
 RT Ca2(+)-storage compartments (calciosomes) of liver and brain.";
 RL Biochem. J. 271:473-480(1990).
 [6]
 RP SEQUENCE OF 18-32.
 RC STRAIN SPRAGUE-DAWLEY; TISSUE: Testis;
 RX MEDLINE-92360010; PubMed-1497655;
 RA Nakamura M., Michikawa Y., Baba T., Okinaga S., Arai K.;
 RT "Calreticulin is present in the acrosome of spermatids of rat
 RT testis.";
 RL Biochem. Biophys. Res. Commun. 186:668-673(1992).
 [7]
 RP SEQUENCE OF 18-32.
 RC STRAIN LEC; TISSUE: Liver;
 RX MEDLINE-94072621; PubMed-8251535;
 RA Yokoi T., Nagayama S., Kajiwara R., Kawaguchi Y., Horiuchi R.,
 RA Kametaki T.;
 RT "Identification of protein disulfide isomerase and calreticulin as
 RT autoantigen antigens in LEC strain of rats.";
 RL Biochim. Biophys. Acta 1158:339-344(1993).
 CC -1- FUNCTION: THIS PROTEIN BINDS CALCIUM. THERE ARE BOTH HIGH AND
 CC LOW AFFINITY CALCIUM-BINDING SITES.
 CC -1- SUBUNIT: MONOMER (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM LUMEN.
 CC -1- SIMILARITY: BELONGS TO THE CALRETICULIN FAMILY.
 CC -1- CAUTION: WAS ORIGINALLY (REF.2) THOUGHT TO BE D-BETA-
 CC HYDROXYBUTYRATE DEHYDROGENASE.

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 DR EMBL: D78308; BA011345.1; -;
 DR EMBL: X53363; CAA37446.1; -;
 DR EMBL: X13702; CAA31987.1; ALT_SEQ.
 DR EMBL: X79347; CAA55890.1; -;
 DR PIR: S04867; S04867.
 DR PIR: S11205; S11205.
 DR PIR: S13045; S13045.
 DR PIR: A49176; A49176.
 DR PIR: S45036; S45036.
 DR PIR: JH0819; JH0819.
 DR InterPro: IPR001580; Calreticulin.
 DR InterPro: IPR000886; ER target.
 DR Pfam: PF00262; calreticulin; 1.
 DR PRINTS: PR00626; CALRETICULIN.
 DR ProDom: PD001866; Calreticulin; 1.
 DR PROSITE: PS00014; ER_TARGET; 1.
 DR PROSITE: PS00803; CALRETICULIN_1; 1.
 DR PROSITE: PS00804; CALRETICULIN_2; 1.

DR PROSITE: PS00805; CALRETICULIN_REPEAT; 3.
 KW Endoplasmic reticulum; Calcium-binding; Repeat; Signal.
 FT SIGNAL 1 17
 FT CHAIN 18 416 CALRETICULIN.
 FT DOMAIN 18 197 N-DOMAIN.
 FT DOMAIN 198 308 P-DOMAIN.
 FT DOMAIN 309 416 C-DOMAIN.
 FT DOMAIN 191 255 4 X APPROXIMATE REPEATS.
 FT REPEAT 191 202 1-1.
 FT REPEAT 210 221 1-2.
 FT REPEAT 227 238 1-3.
 FT REPEAT 244 255 1-4.
 FT DOMAIN 259 297 3 X APPROXIMATE REPEATS.
 FT REPEAT 273 283 2-1.
 FT REPEAT 287 297 2-2.
 FT REPEAT 351 407 ASP/GLU/LYS-RICH.
 FT DISULFID 137 163 BY SIMILARITY.
 FT SITE 413 416 PREVENT SECRETION FROM ER.
 SQ SEQUENCE 416 AA; 47995 MW; 2E6713CED31A2970 CRC64;
 Query Match 98.5%; Score 335; DB 1; Length 416;
 Best Local Similarity 100.0%; Pred. No. 1.4e-33;
 Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 DMHGSEYNIMFGPDICGPGTKKVVHVFNYKGNVINKDKDDEFFHLYTLIVRPDN 61
 DB 121 DMHGSEYNIMFGPDICGPGTKKVVHVFNYKGNVINKDKDDEFFHLYTLIVRPDN 180
 RESULT 5
 CRIC_RABIT
 ID CRIC_RABIT STANDARD; PRT; 418 AA.
 AC P15253;
 DT 01-APR-1990 (Rel. 14, Created)
 DT 01-APR-1990 (Rel. 14, Last sequence update)
 DT 01-OCT-1996 (Rel. 34, Last annotation update)
 DE CALRETICULIN PRECURSOR (CRP55) (CALREGULIN) (HACBP) (BRP60).
 GN CALR.
 OS Oryctolagus cuniculus (Rabbit).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
 OX NCBI_TaxID:9986;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-Slow-twitch skeletal muscle;
 RX MEDLINE-90094320; PubMed-2600080;
 RA Fliegel L., Burns K., MacLennan D.H., Reithmeier R.A.F., Michalak M.;
 RT "Molecular cloning of the high affinity calcium-binding protein
 RT (calreticulin) of skeletal muscle sarcoplasmic reticulum.";
 RL J. Biol. Chem. 264:21522-21528(1989).
 [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE-Fast-twitch skeletal muscle;
 RX MEDLINE-91282795; PubMed-2059224;
 RA Fliegel L., Michalak M.;
 RT "Fast-twitch and slow-twitch skeletal muscles express the same
 RT isoform of calreticulin.";
 RL Biochem. Biophys. Res. Commun. 177:979-984(1991).
 [3]
 RP SEQUENCE OF 18-36.
 RX MEDLINE-91054414; PubMed-2241926;
 RA Treves S., de Mattei M., Lanfredi M., Villa A., Green N.M.,
 RA MacLennan D.H., Meldolesi J., Pozzan T.;
 RT "Calreticulin is a candidate for a calsequestrin-like function in
 RT Ca2(+)-storage compartments (calciosomes) of liver and brain.";
 RL Biochem. J. 271:473-480(1990).
 [4]
 RP SEQUENCE OF 18-46.
 RX MEDLINE-91201375; PubMed-2016321;
 RA Milner R.E., Baksh S., Shemanko C., Carpenter M.R., Smillie L.,
 RA Vance J.E., Opas M., Michalak M.;

"Calreticulin, and not calsequestrin, is the major calcium binding protein of smooth muscle sarcoplasmic reticulum and liver endoplasmic reticulum.";
J. Biol. Chem. 266:7155-7165(1991).
[5]
PARTIAL SEQUENCE.
RC TISSUE=Lung;
RX MEDLINE=92002038; PubMed=1911780;
RA Guan S., Fallick A.M., Williams D.E., Cashman J.R.;
RT "Evidence for complex formation between rabbit lung flavin-containing monooxygenase and calreticulin.";
RL Biochemistry 30:9892-9900(1991).
CC -!- FUNCTION: THIS PROTEIN BINDS CALCIUM. THERE ARE BOTH HIGH AND LOW AFFINITY CALCIUM-BINDING SITES.
CC -!- SUBUNIT: MONOMER (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM LUMEN.
CC -!- SIMILARITY: BELONGS TO THE CALRETICULIN FAMILY.

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DR EMBL; J05138; AAA31188.1; .
DR PIR; A34154; A34154.
DR PIR; C33208; C33208.
DR PIR; D33208; D33208.
DR PIR; E33208; E33208.
DR PIR; F33208; F33208.
DR PIR; S13046; S13046.
DR PIR; S13047; S13047.
DR InterPro; IPR001580; Calreticulin.
DR InterPro; IPR000886; ER.target.
DR Pfam; PF00262; calreticulin; 1.
DR PRINTS; PR00626; CALRETICULIN.
DR PRODOM; PD001866; Calreticulin; 1.
DR PROSITE; PS00014; ER.TARGET; 1.
DR PROSITE; PS00803; CALRETICULIN.1; 1.
DR PROSITE; PS00804; CALRETICULIN.2; 1.
DR PROSITE; PS00805; CALRETICULIN_REPEAT; 3.
KW Endoplasmic reticulum; Calcium-binding; Repeat; Signal.
FT SIGNAL 1 17
FT CHAIN 18 418 CALRETICULIN.
FT DOMAIN 18 197 N-DOMAIN.
FT DOMAIN 198 308 P-DOMAIN.
FT DOMAIN 309 418 C-DOMAIN.
FT REPEAT 191 255 4 X APPROXIMATE REPEATS.
FT REPEAT 210 221 1-1.
FT REPEAT 210 221 1-2.
FT REPEAT 227 238 1-3.
FT REPEAT 244 255 1-4.
FT DOMAIN 259 297 3 X APPROXIMATE REPEATS.
FT REPEAT 259 269 2-1.
FT REPEAT 273 283 2-2.
FT REPEAT 287 297 2-3.
FT DOMAIN 351 408 ASP/GLU/LYS-RICH.
FT DISULFID 137 163 BY SIMILARITY.
FT SITE 415 418 PREVENT SECRETION FROM ER.
FT VARIANT 35 35 E -> D.
FT CONFLICT 90 90 P -> T (IN REF. 5).
SQ SEQUENCE 418 AA; 48275 MW; B6082B689DC763A6 CRC64;

Query Match 98.5%; Score 335; DB 1; Length 418;
Best Local Similarity 100.0%; Pred. No. 1.4e-33;
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DMHGDSEYNMFPGDTCGCTKKVHVIFNYKGNVLINKDIRCKDDEFFHLYTLIVRPDN 61
|||||

DB 121 DMHGDSEYNMFPGDTCGCTKKVHVIFNYKGNVLINKDIRCKDDEFFHLYTLIVRPDN 180
|||||

RESULT 6
CRT2_BOVIN STANDARD; PRT; 421 AA.
ID CRT2_BOVIN
AC P42918;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE CALRETICULIN, BRAIN ISOFORM 2 PRECURSOR (CRP55) (CALREGULIN) (HACBP).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=93385184; PubMed=8373827;
RA Liu N., Fine R.E., Johnson R.J.;
RT "Comparison of cDNAs from bovine brain coding for two isoforms of calreticulin.";
RL Biochim. Biophys. Acta 1202:70-76(1993).
CC -!- FUNCTION: THIS PROTEIN BINDS CALCIUM. THERE ARE BOTH HIGH AND LOW AFFINITY CALCIUM-BINDING SITES.
CC -!- SUBUNIT: MONOMER (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM LUMEN.
CC -!- SIMILARITY: BELONGS TO THE CALRETICULIN FAMILY.

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DR EMBL; L13462; AAC37307.1; .
DR InterPro; IPR001580; Calreticulin.
DR InterPro; IPR000886; ER.target.
DR Pfam; PF00262; calreticulin; 1.
DR PRINTS; PR00626; CALRETICULIN.
DR PRODOM; PD001866; Calreticulin; 1.
DR PROSITE; PS00014; ER.TARGET; 1.
DR PROSITE; PS00803; CALRETICULIN.1; 1.
DR PROSITE; PS00804; CALRETICULIN.2; 1.
DR PROSITE; PS00805; CALRETICULIN_REPEAT; 3.
KW Endoplasmic reticulum; Calcium-binding; Repeat; Signal.
FT SIGNAL 1 34 POTENTIAL.
FT CHAIN 35 421 CALRETICULIN, BRAIN ISOFORM 2.
FT DOMAIN 35 201 N-DOMAIN.
FT DOMAIN 202 312 P-DOMAIN.
FT DOMAIN 313 421 C-DOMAIN.
FT DOMAIN 195 259 4 X APPROXIMATE REPEATS.
FT REPEAT 214 225 1-1.
FT REPEAT 231 242 1-2.
FT REPEAT 248 259 1-3.
FT REPEAT 263 301 1-4.
FT DOMAIN 263 301 3 X APPROXIMATE REPEATS.
FT REPEAT 263 273 2-1.
FT REPEAT 277 287 2-2.
FT REPEAT 291 301 2-3.
FT DOMAIN 366 411 ASP/GLU/LYS-RICH.
FT DISULFID 141 167 BY SIMILARITY.
FT CARBOHYD 183 183 N-LINKED (GLCNAC. .) (POTENTIAL).
FT SITE 418 421 PREVENT SECRETION FROM ER.
SQ SEQUENCE 421 AA; 48812 MW; 0257E959F71528BC CRC64;

Query Match 98.5%; Score 335; DB 1; Length 421;
Best Local Similarity 98.4%; Pred. No. 1.4e-33;
Matches 60; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TDMHGSEYNIMFGPDICGPTGKVKHVIFNYKGNVLINKIRCKDDETHLYTLVRPD 60
 Db 124 TDMHGSEYNIMFGPDICGPTGKVKHVIFNYKGNVLINKIRCKDDETHLYTLVRPN 183
 QY 61 N 61
 Db 184 N 184

RESULT 7
 ID CRTIC_DROME STANDARD; PRT; 406 AA.
 AC P29413; Q9VHA3;
 DT 01-APR-1993 (Rel. 25, Created)
 DT 01-OCT-1993 (Rel. 27, Last sequence update)
 DT 20-AUG-2001 (Rel. 40, Last annotation update)
 DE CALRETICULIN PRECURSOR (CRP55) (CALREGULIN) (HACBP).
 GN CRC OR CG9429.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephygroidae; Drosophilidae; Drosophila.
 OX NCBI_TaxID:7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-93208374; PubMed-1296819;
 RA Smith M.J.;
 RT "Nucleotide sequence of a Drosophila melanogaster gene encoding a
 calreticulin homologue.";
 RL DNA Seq. 3:247-250(1992).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN BERKELEY;
 RX MEDLINE-20196006; PubMed-10731132;
 RA Adams M.D., Celisner S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amaratides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Vandeil M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers J.H.C., Blazer R.G., Champe M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA Ballou R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
 RA Burtis K.C., Busam D.A., Butler H., Cadiou E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Holman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
 RA Julali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacle J.M.,
 RA Paluzzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kimons I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stuppleton M., Strong R., Sun E.,
 RA Swirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wasserman D.A., Weissstock G.M., Weissbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of Drosophila melanogaster.";
 RL Science 287:2185-2195(2000).
 RN [3]

RP SEQUENCE OF 91-124 AND 182-220.
 RX MEDLINE-90307981; PubMed-2365822;
 RA McCaulliffe D.P., Zappi E., Lieu T.S., Michalak M., Sontheimer R.D.,
 RA Capra J.D.;
 RT "A human Ro/SS-A autoantigen is the homologue of calreticulin and is
 RT highly homologous with oncohercal RAL-1 antigen and an alysia
 RT 'memory molecule'.";
 RL J. Clin. Invest. 86:332-335(1990).
 CC -!- FUNCTION: THIS PROTEIN BINDS CALCIUM. THERE ARE BOTH HIGH AND
 CC LOW AFFINITY CALCIUM-BINDING SITES.
 CC -!- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM LUMEN.
 CC -!- SIMILARITY: BELONGS TO THE CALRETICULIN FAMILY.
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 CC -----
 DR EMBL; X64461; CAA45791.1; -;
 DR EMBL; AE003683; AAF54416.1; -;
 DR PIR; A37158; A37158.
 DR FlyBase; FBgn0005585; Crc.
 DR InterPro; IPR001580; Calreticulin.
 DR InterPro; IPR000896; ER_target.
 DR Pfam; PF00262; calreticulin; 1.
 DR PRINTS; PR00626; CALRETICULIN.
 DR ProDom; PD001866; Calreticulin; 1.
 DR PROSITE; PS00014; ER_TARGET; 1.
 DR PROSITE; PS00803; CALRETICULIN_1; 1.
 DR PROSITE; PS00804; CALRETICULIN_2; 1.
 DR PROSITE; PS00805; CALRETICULIN_REPEAT; 3.
 KW Endoplasmic reticulum; Calcium-binding; Repeat; Signal.
 FT SIGNAL 1 17 POTENTIAL.
 FT CHAIN 18 406 CALRETICULIN.
 FT CONFLICT 107 107 G -> A (IN REF. 3).
 FT CONFLICT 184 184 V -> L (IN REF. 3).
 SQ SEQUENCE 406 AA; 46808 MW; 65D72CG9D0BEC427 CRC64;
 Query Match 86.2%; Score 293; DB 1; Length 406;
 Best Local Similarity 85.2%; Pred. NO. 1.8e-28;
 Matches 52; Conservative 4; Mismatches 5; Indels 0; Gaps 0;
 QY 1 TDMHGSEYNIMFGPDICGPTGKVKHVIFNYKGNVLINKIRCKDDETHLYTLVRPD 60
 Db 120 TDMHGSEYNIMFGPDICGPTGKVKHVIFNYKGNVLINKIRCKDDETHLYTLVRPD 179
 QY 61 N 61
 Db 180 N 180

RESULT 8
 ID RALI_ONCVO STANDARD; PRT; 388 AA.
 AC P11012;
 DT 01-JUL-1989 (Rel. 11, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 01-OCT-1996 (Rel. 34, Last annotation update)
 DE RAL-1 PROTEIN PRECURSOR (41 KDA LARVAL ANTIGEN).
 GN RALI.
 OS Onchocerca volvulus.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea;
 OC Onchocercidae; Onchocerca.
 OX NCBI_TaxID:6282;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-94341871; PubMed-7520419;
 RA Rokeach L.A., Zimmerman P.A., Unnasch T.R.;
 RT "Epitopes of the Onchocerca volvulus RALI antigen, a member of the


```
RL Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: THIS PROTEIN BINDS CALCIUM. THERE ARE BOTH HIGH AND
CC LOW AFFINITY CALCIUM-BINDING SITES (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM LUMEN (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE CALRETICULIN FAMILY.
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CC -----
DR EMBL; AJ002057; CAA05161.1; -
DR Mendel; 32549; Betvu:1166;32549.
DR InterPro; IPR001580; Calreticulin.
DR InterPro; IPR000886; ER.target.
DR Pfam; PF00262; calreticulin; 1.
DR PRINTS; PR00626; CALRETICULIN.
DR ProDom; PD001866; Calreticulin; 1.
DR PROSITE; PS00014; ER_TARGET; 1.
DR PROSITE; PS00803; CALRETICULIN_1; 1.
DR PROSITE; PS00804; CALRETICULIN_2; 1.
DR PROSITE; PS00805; CALRETICULIN_REPEAT; 2.
KW Endoplasmic reticulum; Calcium-binding; Repeat; Signal; Glycoprotein.
FT SIGNAL 1 25 POTENTIAL.
FT CHAIN 26 416 CALRETICULIN.
FT CARBOHYD 57 57 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 157 157 N-LINKED (GLCNAC. .) (POTENTIAL).
FT SITE 413 416 PREVENT SECRETION FROM ER (POTENTIAL).
SQ SEQUENCE 416 AA; 48136 MW; 565FEC3489F77CA7 CRC64;

Query Match 60.9%; Score 207; DB 1; Length 416;
Best Local Similarity 64.3%; Pred No. 5,9e-18;
Matches 36; Conservative 7; Mismatches 13; Indels 0; Gaps 0;

QY 5 GDSYNNMFPGDPCGKTKVHFNKGNVNLINKDKDETHLYTLIVRPD 60
Db 130 GDTYSIMFGPDICGYSYKVKHAIENYNTNHLKKDVPCTDQLTHVTVFIIRPD 185

RESULT 13
CRTC_PRUAR
ID CRTC_PRUAR STANDARD; PRT; 421 AA.
AC Q9XF98;
DT 20-AUG-2001 (Rel. 40, Created)
DT 20-AUG-2001 (Rel. 40, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE CALRETICULIN PRECURSOR.
OS Prunus armeniaca (Apricot).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids I; Rosales; Rosaceae; Prunus.
OX NCBI_TaxID=36596;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97435975; PubMed=9290642;
RA Coughlan S.J., Hastings C., Winfrey R. Jr.;
RT "Cloning and characterization of the calreticulin gene from Ricinus
RT communis L.";
RL Plant Mol. Biol. 34:897-911(1997).
CC -!- FUNCTION: THIS PROTEIN BINDS CALCIUM. THERE ARE BOTH HIGH AND
CC LOW AFFINITY CALCIUM-BINDING SITES.
CC -!- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM LUMEN.
CC -!- SIMILARITY: BELONGS TO THE CALRETICULIN FAMILY.
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CC -----
DR EMBL; U74631; AAB71420.1; -
DR EMBL; U74630; AAB71419.1; -
DR Mendel; 10452; Ricco:1166;10452.
DR InterPro; IPR001580; Calreticulin.
DR InterPro; IPR000886; ER.target.
DR Pfam; PF00262; calreticulin; 1.
DR PRINTS; PR00626; CALRETICULIN.
DR ProDom; PD001866; Calreticulin; 1.
DR PROSITE; PS00014; ER_TARGET; 1.
DR PROSITE; PS00803; CALRETICULIN_1; 1.
DR PROSITE; PS00804; CALRETICULIN_2; 1.
DR PROSITE; PS00805; CALRETICULIN_REPEAT; 2.
KW Endoplasmic reticulum; Calcium-binding; Repeat; Signal; Glycoprotein.
FT SIGNAL 1 22 POTENTIAL.
FT CHAIN 23 421 CALRETICULIN.
FT CARBOHYD 56 56 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 156 156 N-LINKED (GLCNAC. .) (POTENTIAL).
FT SITE 418 421 PREVENT SECRETION FROM ER (POTENTIAL).
SQ SEQUENCE 421 AA; 48416 MW; 4F5F94CBAA6C6690 CRC64;
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CC -----
DR EMBL; AF134733; AAD32207.1; -
DR InterPro; IPR001580; Calreticulin.
DR InterPro; IPR000886; ER.target.
DR Pfam; PF00262; calreticulin; 1.
DR PRINTS; PR00626; CALRETICULIN.
DR ProDom; PD001866; Calreticulin; 1.
DR PROSITE; PS00014; ER_TARGET; 1.
DR PROSITE; PS00803; CALRETICULIN_1; 1.
DR PROSITE; PS00804; CALRETICULIN_2; 1.
DR PROSITE; PS00805; CALRETICULIN_REPEAT; 2.
KW Endoplasmic reticulum; Calcium-binding; Repeat; Signal; Glycoprotein.
FT SIGNAL 1 22 POTENTIAL.
FT CHAIN 23 421 CALRETICULIN.
FT CARBOHYD 56 56 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 156 156 N-LINKED (GLCNAC. .) (POTENTIAL).
FT SITE 418 421 PREVENT SECRETION FROM ER (POTENTIAL).
SQ SEQUENCE 421 AA; 48416 MW; 4F5F94CBAA6C6690 CRC64;

Query Match 60.0%; Score 204; DB 1; Length 421;
Best Local Similarity 62.5%; Pred No. 1.4e-17;
Matches 35; Conservative 7; Mismatches 14; Indels 0; Gaps 0;

QY 5 GDSYNNMFPGDPCGKTKVHFNKGNVNLINKDKDETHLYTLIVRPD 60
Db 129 GDTYSIMFGPDICGYSYKVKHAILNNTNNTNHLKKDVPCTDQLTHVTVFIIRPD 184

RESULT 14
CRTC_RICCO
ID CRTC_RICCO STANDARD; PRT; 415 AA.
AC P93508;
DT 20-AUG-2001 (Rel. 40, Created)
DT 20-AUG-2001 (Rel. 40, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE CALRETICULIN PRECURSOR.
OS Ricinus communis (Castor bean).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids I; Malpighiales; Euphorbiaceae; Ricinus.
OX NCBI_TaxID=3988;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97435975; PubMed=9290642;
RA Coughlan S.J., Hastings C., Winfrey R. Jr.;
RT "Cloning and characterization of the calreticulin gene from Ricinus
RT communis L.";
RL Plant Mol. Biol. 34:897-911(1997).
CC -!- FUNCTION: THIS PROTEIN BINDS CALCIUM. THERE ARE BOTH HIGH AND
CC LOW AFFINITY CALCIUM-BINDING SITES.
CC -!- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM LUMEN.
CC -!- SIMILARITY: BELONGS TO THE CALRETICULIN FAMILY.
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CC -----
DR EMBL; U74631; AAB71420.1; -
DR EMBL; U74630; AAB71419.1; -
DR Mendel; 10452; Ricco:1166;10452.
DR InterPro; IPR001580; Calreticulin.
DR InterPro; IPR000886; ER.target.
DR Pfam; PF00262; calreticulin; 1.
DR PRINTS; PR00626; CALRETICULIN.
DR ProDom; PD001866; Calreticulin; 1.
DR PROSITE; PS00014; ER_TARGET; 1.
DR PROSITE; PS00803; CALRETICULIN_1; 1.
DR PROSITE; PS00804; CALRETICULIN_2; 1.
DR PROSITE; PS00805; CALRETICULIN_REPEAT; 2.
KW Endoplasmic reticulum; Calcium-binding; Repeat; Signal; Glycoprotein.
FT SIGNAL 1 22 POTENTIAL.
FT CHAIN 23 421 CALRETICULIN.
FT CARBOHYD 56 56 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 156 156 N-LINKED (GLCNAC. .) (POTENTIAL).
FT SITE 418 421 PREVENT SECRETION FROM ER (POTENTIAL).
SQ SEQUENCE 421 AA; 48416 MW; 4F5F94CBAA6C6690 CRC64;
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SUMMARIES						
Result No.	Score	Query %		DB	ID	Description
		Match	Length			
1	309	90.9	421	5	Q9U6S0	Q9U6S0 stronglylce
2	305	89.7	405	5	Q26268	Q26268 aplysia cal
3	303	89.1	318	13	Q9PRX7	Q9PRX7 lampetra re
4	296	87.1	343	13	Q91711	Q91711 xenopus lae
5	293	86.2	406	5	Q9U916	Q9U916 drosophila
6	288	84.7	411	13	Q91710	Q91710 xenopus lae
7	287	84.4	419	13	Q98984	Q98984 rana rugosa
8	281	82.6	410	5	Q16893	Q16893 amblyomma a
9	274	80.6	387	5	Q97372	Q97372 dirofilaria
10	270	79.4	417	13	Q9PUC1	Q9PUC1 brachydanio
11	269	79.1	375	5	Q18478	Q18478 litomosoides
12	261.5	76.9	403	5	Q76961	Q76961 necator ame
13	250	73.5	350	5	Q26514	Q26514 schistosoma
14	250	73.5	396	5	Q45034	Q45034 schistosoma
15	230	67.6	321	13	Q9U560	Q9U560 eptatretus
16	205	60.3	321	10	Q41799	Q41799 zea mays (m
17	205	60.3	421	10	Q43712	Q43712 zea mays (m
18	200	58.8	412	10	Q40040	Q40040 hordeum vul
19	200	58.8	415	10	Q40041	Q40041 hordeum vul

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RESULT 2
Q26268 ID Q26268 PRELIMINARY; PRT; 405 AA.
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE CALRETICULIN
OS Aplysia californica (California sea hare).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Opisthobranchia; Anaspidea;
OC Aplousididae; Aplysia.
OX NCBI_TaxID:6500;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-93098937; PubMed 1463604;
RA Kennedy T.E., Kuhl D., Barrilal A., Sweatt J.D., Kandel E.R.;
RT "Long-term sensitization training in Aplysia leads to an increase in
calreticulin, a major presynaptic calcium-binding protein.";
RL Neuron 9:1013-1024(1992).
DR EMBL: S51239; AAB24569.1; -
DR InterPro: IPR000886; ER.target.
DR InterPro: IPR001580; Calreticulin.
DR Pfam: PF00262; calreticulin; 1.
DR PRINTS: PR00626; Calreticulin.
DR ProDom: PD001866; Calreticulin; 1.
DR PROSITE: PS00803; CALRETICULIN_1; 1.
DR PROSITE: PS00804; CALRETICULIN_2; 1.
DR PROSITE: PS00805; CALRETICULIN_REPEAT; 3.
DR PROSITE: PS00014; ER_TARGET; UNKNOWN_1.
SQ SEQUENCE 405 AA; 46738 MW; 14CAA201840D1D69 CRC64;

Query Match 89.7%; Score 305; DB 5; Length 405;
Best Local Similarity 86.9%; Pred. No. 5e-29;
Matches 53; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 1 TMHGDSEYNIMFGPDICGPGTKKVVHVIYFKGNVLINKDIRCKDDETHLYTLIVRPD 60
Db 116 SDMHGSEYNIMFGPDICGPGTKKVVHVIYFKGNVLINKDIRCKDDVFSHLYTLIVRPD 175

QY 61 N 61
Db 176 N 176

RESULT 3
Q9PTX7 ID Q9PTX7 PRELIMINARY; PRT; 318 AA.
AC Q9PTX7
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE CALRETICULIN (FRAGMENT).
OS Lampetia roissneri.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Hyperoartia;
OC Petromyzontiformes; Petromyzontidae; Lampetra.
OX NCBI_TaxID:7753;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-20063780; PubMed-10594174;
RA Kuraku S., Hoshiyama D., Katoh K., Suga H., Miyata T.;
RT "Monophyly of lampreys and hagfishes supported by nuclear DNA-coded
genes.";
RL J. Mol. Evol. 49:729-735(1999).
DR EMBL: AB025328; BAA88481.1; -
DR InterPro: IPR000886; ER.target.
DR InterPro: IPR001580; Calreticulin.
DR Pfam: PF00262; Calreticulin; 1.
DR PRINTS: PR00626; Calreticulin.
DR ProDom: PD001866; Calreticulin; 1.
DR PROSITE: PS00804; CALRETICULIN_2; 1.

Query Match 87.1%; Score 296; DB 13; Length 343;
Best Local Similarity 86.9%; Pred. No. 5.2e-28;
Matches 53; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 TMHGDSEYNIMFGPDICGPGTKKVVHVIYFKGNVLINKDIRCKDDETHLYTLIVRPD 60
Db 92 TEMHGESEYNIMFGPDICGPGTKKVVHVIYFKGNVLINKDIRCKDDSFTHLYTLIVRPD 151

QY 61 N 61
Db 152 N 152

RESULT 5
Q9U916 ID Q9U916 PRELIMINARY; PRT; 406 AA.
AC Q9U916;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE CALRETICULIN
OS Drosophila melanogaster (Fruit fly).
OS Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

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OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=OREGON-R;
RA Dodo K., Sakoyama Y., Gamo S.;
RT "Drosophila melanogaster calreticulin for mRNA.";
RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB000718; BAA85379.1; -.
DR FlyBase; FBgn0005585; Crc.
DR InterPro; IPR001580; Calreticulin.
DR InterPro; IPR000886; ER_target.
DR Pfam; PF00262; calreticulin; 1.
DR PRINTS; PR00626; CALRETICULIN.
DR ProDom; PD001866; Calreticulin; 1.
DR PROSITE; PS00803; CALRETICULIN_1; 1.
DR PROSITE; PS00804; CALRETICULIN_2; 1.
DR PROSITE; PS00805; CALRETICULIN_REPEAT; 3.
DR PROSITE; PS00014; ER_TARGET; UNKNOWN_1.
SQ SEQUENCE 406 AA; 46809 MW; 68BA49A6B81CC427 CRC64;

Query Match 86.2%; Score 293; DB 5; Length 406;
Best Local Similarity 85.2%; Pred. No. 1.4e-27;
Matches 52; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 1 TDMHGDSEYNIMFGPDICGPGTKKVVHVFYNYGKNNVLINKDKDDETHLYTLIVRPD 60
DB 120 TDMHGESYEIMFGPDICGPGTKKVVHVFYNYGKNNLISKDKDDVYTHYTLIVRPD 179

QY 61 N 61
DB 180 N 180

RESULT 6
QY1710 ID Q91710 PRELIMINARY; PRT; 411 AA.
AC Q91710;
DT 01-JAN-1998 (TReMBLrel. 05, Created)
DT 01-JAN-1998 (TReMBLrel. 05, Last sequence update)
DE 01-JUN-2001 (TReMBLrel. 17, Last annotation update)
DE CALRETICULIN PRECURSOR (FRAGMENT).
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=BRAIN;
RX MEDLINE=93074997; PubMed=1445218;
RA Treves S., Zorzato F., Pozzan T.;
RT "Identification of calreticulin isoforms in the central nervous
RT system.";
RL Biochem. J. 287:579-581(1992).
DR EMBL; X67597; CAA47866.1; -.
DR InterPro; IPR000886; ER_target.
DR InterPro; IPR001580; Calreticulin.
DR Pfam; PF00262; calreticulin; 1.
DR PRINTS; PR00626; CALRETICULIN.
DR ProDom; PD001866; Calreticulin; 1.
DR PROSITE; PS00803; CALRETICULIN_1; 1.
DR PROSITE; PS00804; CALRETICULIN_2; 1.
DR PROSITE; PS00805; CALRETICULIN_REPEAT; 2.
DR PROSITE; PS00014; ER_TARGET; UNKNOWN_1.
KW Signal.
FT NON_TER 1
FT SIGNAL <1 12 POTENTIAL.
FT CHAIN 13 411 CALRETICULIN.
FT SEQUENCE 411 AA; 48344 MW; 891DA66E00EBEFA CRC64;

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Query Match 84.7%; Score 288; DB 13; Length 411;
Best Local Similarity 85.2%; Pred. No. 5.9e-27;
Matches 52; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 1 TDMHGDSEYNIMFGPDICGPGTKKVVHVFYNYGKNNVLINKDKDDETHLYTLIVRPD 60
DB 115 TMHGESEYNIMFGPDICGPGTKKVVHVFYNYGKNNLQINKDKDSDSFTHLYTLIVRPD 174

QY 61 N 61
DB 175 N 175

RESULT 7
QY9894 ID Q9894 PRELIMINARY; PRT; 419 AA.
AC Q9894;
DT 01-FEB-1997 (TReMBLrel. 02, Created)
DT 01-FEB-1997 (TReMBLrel. 02, Last sequence update)
DT 01-JUN-2001 (TReMBLrel. 17, Last annotation update)
DE CALRETICULIN.
OS Rana rugosa (Frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Rana.
OX NCBI_TaxID=8410;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96234004; PubMed=8654561;
RA Yamamoto S., Nakamura M.;
RT "Calnexin: its molecular cloning and expression in the liver of the
RT frog, Rana rugosa.";
RL FEBS Lett. 387:27-32(1996).
RN [2]
RP SEQUENCE FROM N.A.
RA Yamamoto S.;
RT "Strong expression of the calreticulin gene in the liver of Rana
RT rugosa Tadpoles.";
RL J. Exp. Zool. 0:0-0(1996).
DR EMBL; D78589; BAA11425.1; -.
DR InterPro; IPR000886; ER_target.
DR InterPro; IPR001580; Calreticulin.
DR Pfam; PF00262; calreticulin; 1.
DR PRINTS; PR00626; CALRETICULIN.
DR ProDom; PD001866; Calreticulin; 1.
DR PROSITE; PS00803; CALRETICULIN_1; 1.
DR PROSITE; PS00804; CALRETICULIN_2; 1.
DR PROSITE; PS00805; CALRETICULIN_REPEAT; 3.
DR PROSITE; PS00014; ER_TARGET; UNKNOWN_1.
SQ SEQUENCE 419 AA; 48658 MW; 2C857036769673BF CRC64;

Query Match 84.4%; Score 287; DB 13; Length 419;
Best Local Similarity 85.2%; Pred. No. 8e-27;
Matches 52; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 1 TDMHGDSEYNIMFGPDICGPGTKKVVHVFYNYGKNNVLINKDKDDETHLYTLIVRPD 60
DB 121 TMHGESEYNIMFGPDICGPGTKKVVHVFYNYGKNNLQINKDKADVYSHLYTLIVRPD 180

QY 61 N 61
DB 181 N 181

RESULT 8
QY16893 ID Q16893 PRELIMINARY; PRT; 410 AA.
AC Q16893;
DT 01-NOV-1996 (TReMBLrel. 01, Created)
DT 01-JAN-1999 (TReMBLrel. 09, Last sequence update)
DT 01-JUN-2001 (TReMBLrel. 17, Last annotation update)
DE CALRETICULIN.

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GN CRT-1.
 OS Amblyomma americanum.
 OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Acari;
 OC Parasitiformes; Ixodida; Ixodidae; Amblyomma.
 OX NCBI_TaxID:6943;
 RN [1]
 RP SEQUENCE OF 49-410 FROM N.A.
 RC TISSUE SALIVARY GLANDS;
 RA Jaworski D.C.; Simmen F.A.; Lamoreaux W.J.; Coons L.B.; Muller M.T.;
 RA Needham G.R.;
 RT "A secreted calreticulin protein in Ixodid tick (Amblyomma americanum)
 RT saliva";
 RL J. Insect Physiol. 41:369-375(1995).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE SALIVARY GLANDS;
 RA Juorinki D.C.;
 RL Submitted (MAR-1994) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE SALIVARY GLANDS;
 RA Fain-Thornton J.M.; Jaworski D.C.; Needham G.R.;
 RL Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL; U07708; AAC79094.1; -.
 DR Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
 DR InterPro; IPR000886; ER_target.
 DR Cypriniformes; Cyprinidae; Rasbora; Danio.
 DR Pfam; PF00262; Calreticulin; 1.
 DR PRINTS; PR00626; CALRETICULIN.
 DR ProDom; PD001866; Calreticulin; 1.
 DR PROSITE; PS00803; CALRETICULIN_1; 1.
 DR PROSITE; PS00805; CALRETICULIN_REPEAT; 3.
 DR PROSITE; PS00014; ER_TARGET; UNKNOWN_1.
 DR SEQUENCE 410 AA; 47485 MW; 32CCB8750A17DC54 CRC64;
 SQ
 Query Match 82.6%; Score 281; DB 5; Length 410;
 Best Local Similarity 84.7%; Pred. No. 4.2e-26;
 Matches 50; Conservative 4; Mismatches 5; Indels 0; Gaps 0;
 QY 3 MHGDSYNIIMFGPDICGPGTKKVVHVFYKGNVINKDIRCKDDFTHTLYLIVRPD 61
 DB 121 LHGESPKIMFPPDIPGPGTKKVVHVFYKGNVINKDIRCKDDFTHTLYLIVRPD 179
 RESULT 9
 QY7372 ID QY7372 PRELIMINARY; PRT; 387 AA.
 AC QY7372
 DT 01-MAY-1999 (TREMBlrel. 10, Created)
 DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)
 DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
 DE CALRETICULIN PRECURSOR.
 OS Dirofilaria immitis.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea;
 OC Onchocercidae; Dirofilaria.
 OX NCBI_TaxID:6287;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE 90094497; PubMed:9879888;
 RA Tsuji N., Morales T.H., Ozols V.V., Carmody A.B., Chandrashekar R.;
 RT "Molecular characterization of a calcium-binding protein from the
 RT filarial parasite Dirofilaria immitis";
 RL Mol. Biochem. Parasitol. 97:69-79(1998).
 DR EMBL; AF052978; AAD03405.1; -.
 DR InterPro; IPR001580; Calreticulin.
 DR Pfam; PF00262; calreticulin; 1.
 DR PRINTS; PR00626; CALRETICULIN.
 DR ProDom; PD001866; Calreticulin; 1.
 DR PROSITE; PS00803; CALRETICULIN_1; 1.
 DR PROSITE; PS00804; CALRETICULIN_2; 1.
 DR PROSITE; PS00805; CALRETICULIN_REPEAT; 3.
 KW Signal.
 FT SIGNAL 1 18 POTENTIAL.

FT CHAIN 19 387 CALRETICULIN.
 SQ SEQUENCE 387 AA; 44941 MW; E7741BF6AAFA5885 CRC64;
 Query Match 80.6%; Score 274; DB 5; Length 387;
 Best Local Similarity 80.0%; Pred. No. 2.8e-25;
 Matches 48; Conservative 5; Mismatches 7; Indels 0; Gaps 0;
 QY 2 DMHGDSYNIIMFGPDICGPGTKKVVHVFYKGNVINKDIRCKDDFTHTLYLIVRPD 61
 DB 119 DFHGETPYNIMFGPDICGPGTKKVVHVFYKGNVINKDIRCKDDFTHTLYLIVRPN 178
 RESULT 10
 QY7372 ID QY7372 PRELIMINARY; PRT; 417 AA.
 AC QY7372
 DT 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
 DE CALRETICULIN.
 OS Brachydanio rerio (zebrafish) (Zebra danio).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
 OC Cypriniformes; Cyprinidae; Rasbora; Danio.
 OX NCBI_TaxID:7955;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Rubinstein A.L.; Lee D.; Luo R.; Henion P.D.; Halpern M.E.;
 RT "Genes Dependent on zebrafish cyclops Function Identified by AFLP
 RT Differential Gene Expression Screen";
 RL Genesis 0:0-0(1999)
 DR EMBL; AF195882; AAF13700.1; -.
 DR InterPro; IPR000886; ER_target.
 DR Pfam; PF00262; calreticulin; 1.
 DR PRINTS; PR00626; CALRETICULIN.
 DR ProDom; PD001866; Calreticulin; 1.
 DR PROSITE; PS00803; CALRETICULIN_1; 1.
 DR PROSITE; PS00804; CALRETICULIN_2; 1.
 DR PROSITE; PS00805; CALRETICULIN_REPEAT; 3.
 DR PROSITE; PS00014; ER_TARGET; UNKNOWN_1.
 DR SEQUENCE 417 AA; 48723 MW; 2000C5B4004699B6 CRC64;
 SQ
 Query Match 79.4%; Score 270; DB 13; Length 417;
 Best Local Similarity 80.0%; Pred. No. 9.2e-25;
 Matches 48; Conservative 6; Mismatches 6; Indels 0; Gaps 0;
 QY 1 TOMHGDSEYNIIMFGPDICGPGTKKVVHVFYKGNVINKDIRCKDDFTHTLYLIVRPD 60
 DB 120 TEMHGESYIIMFGPDICGPGTKKVVHVFYKGNVINKDIRCKDDFTHTLYLIVRPD 179
 RESULT 11
 QY7372 ID QY7372 PRELIMINARY; PRT; 375 AA.
 AC QY7372
 DT 01-JAN-1998 (TREMBlrel. 05, Created)
 DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)
 DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
 DE RAL-1 PROTEIN (FRAGMENT).
 OS Litomosoides sigmodontis.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea;
 OC Onchocercidae; Litomosoides.
 OX NCBI_TaxID:42156;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MacLennan K., Hoffman W.H., Taylor D.W.;
 RL Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AJ001621; CAA04877.1; -.
 DR InterPro; IPR001580; Calreticulin.
 DR Pfam; PF00262; calreticulin; 1.


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DR PRINTS; PR00626; CALRETICULIN.
DR ProDom; PD001866; Calreticulin; 1.
DR PROSITE; PS00803; CALRETICULIN_1; 1.
DR PROSITE; PS00804; CALRETICULIN_2; 1.
DR PROSITE; PS00805; CALRETICULIN_REPEAT; 3.
FT NON_TER 375
SQ SEQUENCE 375 AA; 43842 MW; 03F7642FBFF7A5B8 CRC64;

Query Match 79.1%; Score 269; DB 5; Length 375;
Best Local Similarity 78.3%; Pred. No. 1.le-24;
Matches 47; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

Qy 2 DMHGSEYNMFGPDICGPGTKVHVIFNYKGNVLINKDIRCKDDETHLYTLIVRPD 61
Db 119 DFHGETPYHIMFGPDICGPGTKVHVIFNYKGRNHMIKKDIRCKDDVETHLYTLIVNSDN 178

RESULT 12
O76961 ID O76961 PRELIMINARY; PRT; 403 AA.
AC O76961;
DT 01-NOV-1998 (TremBLrel. 08, Created)
DT 01-NOV-1998 (TremBLrel. 08, Last sequence update)
DT 01-JUN-2001 (TremBLrel. 17, Last annotation update)
DE CALRETICULIN PRECURSOR.
GN CRT.
OS Necator americanus.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Strongylida;
OC Ancylostomatidae; Ancylostomatidae; Bunostominae; Necator.
OX NCBI_TaxID=51031;
RN [1]
RP SEQUENCE FROM N.A.
RA Pritchard D.I., Brown A., McElroy P., Loukas A., Girdwood K.,
RA Berry C., Fullkrug R., Beck E.;
RT "Calreticulin is a hookworm allergen.";
RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ006790; CAA07234.1; -.
DR InterPro; IPR000886; ER_target.
DR InterPro; IPR001580; Calreticulin.
DR Pfam; PF00262; calreticulin; 1.
DR PRINTS; PR00626; CALRETICULIN.
DR ProDom; PD001866; Calreticulin; 1.
DR PROSITE; PS00803; CALRETICULIN_1; 1.
DR PROSITE; PS00804; CALRETICULIN_2; 1.
DR PROSITE; PS00805; CALRETICULIN_REPEAT; 3.
DR PROSITE; PS00014; ER_TARGET; UNKNOWN_1.
KW Signal; Allergen.
FT SIGNAL 1
FT SIGNAL 16 POTENTIAL.
SQ SEQUENCE 403 AA; 46833 MW; 21F3850515487B6F CRC64;

Query Match 76.9%; Score 261.5; DB 5; Length 403;
Best Local Similarity 77.0%; Pred. No. 9.5e-24;
Matches 47; Conservative 6; Mismatches 7; Indels 1; Gaps 1;

Qy 1 TDMHGSEYNMFGPDICGPGTKVHVIFNYKGNVLINKDIRCKDDETHLYTLIVRPD 60
Db 117 SDFHGETPYNWMFGPDICGPGTKVHVIFSYKGNHLLIKKDIRCKDDELTHLYTLINPD 175

Qy 61 N 61
Db 176 N 176

RESULT 13
Q26514 ID Q26514 PRELIMINARY; PRT; 350 AA.
AC Q26514;
DT 01-NOV-1996 (TremBLrel. 01, Created)
DT 01-NOV-1996 (TremBLrel. 01, Last sequence update)
DT 01-JUN-2001 (TremBLrel. 17, Last annotation update)
DE CALRETICULIN (FRAGMENT).

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GN RAL-1.
OS Schistosoma japonicum (Blood fluke).
OC Eukaryota; Metazoa; Platyhelminthes; Rhabditophora; Neodermata;
OC Trematoda; Digenea; Strigeidida; Schistosomatidae; Schistosomatidae;
OC Schistosoma.
OX NCBI_TaxID=6182;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CHINESE;
RA Huggins M.C., Moloney N.A.;
RL Submitted (AUG-1993) to the EMBL/GenBank/DBJ databases.
DR EMBL; M80524; AAA29517.1; -.
DR InterPro; IPR000886; ER_target.
DR InterPro; IPR001580; Calreticulin.
DR Pfam; PF00262; calreticulin; 1.
DR PRINTS; PR00626; CALRETICULIN.
DR ProDom; PD001866; Calreticulin; 1.
DR PROSITE; PS00803; CALRETICULIN_1; 1.
DR PROSITE; PS00804; CALRETICULIN_2; 1.
DR PROSITE; PS00805; CALRETICULIN_REPEAT; 1.
DR PROSITE; PS00014; ER_TARGET; UNKNOWN_1.
FT NON_TER 1
SQ SEQUENCE 350 AA; 40385 MW; 30FAB4E8BB685D1C CRC64;

Query Match 73.5%; Score 250; DB 5; Length 350;
Best Local Similarity 75.9%; Pred. No. 2e-22;
Matches 44; Conservative 6; Mismatches 8; Indels 0; Gaps 0;

Qy 4 HGDSEYNMFGPDICGPGTKVHVIFNYKGNVLINKDIRCKDDETHLYTLIVRPD 61
Db 76 HGETPYKIMFGPDICGPGTKVHVIFNYKGNHLLIKKDIRCKDDQKTHLYTLIVRPD 133

RESULT 14
O45034 ID O45034 PRELIMINARY; PRT; 396 AA.
AC O45034;
DT 01-JUN-1998 (TremBLrel. 06, Created)
DT 01-JUN-1998 (TremBLrel. 06, Last sequence update)
DT 01-JUN-2001 (TremBLrel. 17, Last annotation update)
DE CALRETICULIN.
OS Schistosoma japonicum (Blood fluke).
OC Eukaryota; Metazoa; Platyhelminthes; Rhabditophora; Neodermata;
OC Trematoda; Digenea; Strigeidida; Schistosomatidae; Schistosomatidae;
OC Schistosoma.
OX NCBI_TaxID=6182;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PHILIPPINE (MINDORO);
RA Scott J.C.;
RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF044408; AAC00515.1; -.
DR InterPro; IPR000886; ER_target.
DR InterPro; IPR001580; Calreticulin.
DR Pfam; PF00262; calreticulin; 1.
DR PRINTS; PR00626; CALRETICULIN.
DR ProDom; PD001866; Calreticulin; 1.
DR PROSITE; PS00803; CALRETICULIN_1; 1.
DR PROSITE; PS00804; CALRETICULIN_2; 1.
DR PROSITE; PS00805; CALRETICULIN_REPEAT; 2.
DR PROSITE; PS00014; ER_TARGET; UNKNOWN_1.
SQ SEQUENCE 396 AA; 45813 MW; C57394C6FB4CD77B CRC64;

Query Match 73.5%; Score 250; DB 5; Length 396;
Best Local Similarity 75.9%; Pred. No. 2.3e-22;
Matches 44; Conservative 6; Mismatches 8; Indels 0; Gaps 0;

Qy 4 HGDSEYNMFGPDICGPGTKVHVIFNYKGNVLINKDIRCKDDETHLYTLIVRPD 61
Db 122 HGETPYKIMFGPDICGPGTKVHVIFNYKGNHLLIKKDIRCKDDQKTHLYTLIVRPD 179

```

```
RESULT 15
Q9U5G0
ID Q9U5G0 PRELIMINARY; PRT; 321 AA.
AC Q9U5G0;
DT 01-MAY-2000 (TRENBLREL. 13, Created)
DT 01-MAY-2000 (TRENBLREL. 13, Last sequence update)
DT 01-JUN-2001 (TRENBLREL. 17, Last annotation update)
DE CALRETICULIN (FRAGMENT).
OS Eptatritus burgeri (Inshore hagfish).
OC Eukaryota; Metazoa; Chordata; Craniata; Hyperotreti; Myxiniiformes;
OC Myxiniidae; Eptatretinae; Eptatretus.
OX NCHI_TaxID:7764;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE: LIVER;
RX MEDLINE:20063780; PubMed 10594174;
RA Kuraku S., Hoshiyama D., Katoh K., Suga H., Miyata T.;
RT "Monophyly of lampreys and hagfishes supported by nuclear DNA-coded
RT genes.";
RL J. Mol. Evol. 49:729-735(1999).
DR EMBL; AH025323; BAA88476.1; -.
DR InterPro; IPR000886; ER_target.
DR InterPro; IPR001580; Calreticulin.
DR Pfam; PF00262; calreticulin; 1.
DR PRINTS; PR00626; CALRETICULIN.
DR PRODOM; PD001866; Calreticulin; 1.
DR PROSITE; PS00804; CALRETICULIN_2; 1.
DR PROSITE; PS00805; CALRETICULIN_REPEAT; 3.
DR PROSITE; PS00014; ER_TARGET; UNKNOWN_1.
PT NON_TER
PT 1
SQ SEQUENCE 321 AA; 37367 MW; 6E8DFA98D42F7AEF CRC64;
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Query Match 67.6%; Score 230; DB 13; Length 321;
Best Local Similarity 70.7%; Pred. No. 4.9e-20;
Matches 41; Conservative 8; Mismatches 9; Indels 0; Gaps 0;

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QY 3 MNGDSEYNIHFGPDICGPGTKKVVHVFNYKGNVLINKDIRCKDDFFTHLYTLIVRPD 60
DB 21 LAGESEYIIMFGPDICGPGTKKVVHVLNSKGNHLIKKEVKCKDDDMTHLYTLMLYPD 78
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Search completed: January 9, 2002, 15:03:28
Job time: 270 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 9, 2002, 15:01:12 ; Search time 83.2 Seconds
(without alignments)
54.309 Million cell updates/sec

Title: US-09-828-000-4
Perfect score: 340
Sequence: 1 TDMHGEYINMGPDICGP.....IRKDKDETHLYTLIVRPDN 61

Scoring table:
BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 522463 seqs, 74073290 residues

Total number of hits satisfying chosen parameters: 522463

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_1101.*
1: /SID88/gcgdata/geneseq/geneseqp/AA1980.DAT.*
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22: /SID88/gcgdata/geneseq/geneseqp/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	340	100.0	180	21	Human vasostatin (
2	340	100.0	400	21	Recombinant human
3	340	100.0	417	10	60 KD Ro (Ro/SSA)
4	340	100.0	417	20	Calreticulin. Hom
5	340	100.0	417	21	Human MBP-calretic
6	335	98.5	401	18	Calreticulin. Hom
7	290	85.3	403	17	Flea calreticulin
8	261	76.8	336	12	Partial sequence o
9	244	71.8	61	21	Recombinant human
10	235	69.1	60	21	Recombinant human
11	235	69.1	280	21	Recombinant delta-

12	202	59.4	415	22	AAB66341	Castor bean calret
13	202	59.4	415	22	AAB66343	Castor bean calret
14	194	57.1	312	21	AAG24609	Arabiopsis thalia
15	194	57.1	312	21	AAG47933	Arabiopsis thalia
16	194	57.1	332	21	AAG30998	Arabiopsis thalia
17	194	57.1	421	21	AAG24608	Arabiopsis thalia
18	194	57.1	421	21	AAG47932	Arabiopsis thalia
19	194	57.1	424	21	AAG24607	Arabiopsis thalia
20	194	57.1	424	21	AAG47931	Arabiopsis thalia
21	194	57.1	441	21	AAG30997	Arabiopsis thalia
22	194	57.1	444	21	AAG30996	Arabiopsis thalia
23	187	55.0	385	21	AAB32385	Human secreted pro
24	175	51.5	49	21	AA192353	Recombinant human
25	125.5	36.9	542	22	AAB66342	Castor bean calnex
26	120.5	35.4	593	16	AA171094	Calnexin sequence.
27	115.5	34.0	530	21	AAG26284	Arabiopsis thalia
28	115.5	34.0	530	21	AAG46611	Arabiopsis thalia
29	115.5	34.0	567	21	AAG46610	Arabiopsis thalia
30	107	31.5	122	20	AA100924	Human cClqR bindin
31	107	31.5	122	20	AA100926	Rat cClqR binding
32	106	31.2	417	21	AA177953	A. thaliana enviro
33	105.5	31.0	532	21	AAG04448	Arabiopsis thalia
34	105.5	31.0	548	21	AAG04447	Arabiopsis thalia
35	99	29.1	122	20	AA100925	Mouse cClqR bindin
36	98.5	29.0	394	21	AAG26285	Arabiopsis thalia
37	98.5	29.0	394	21	AAG46612	Arabiopsis thalia
38	84.5	24.9	394	21	AAG04449	Arabiopsis thalia
39	67.5	19.9	455	21	AAG17438	Arabiopsis thalia
40	67.5	19.9	455	21	AAG21851	Arabiopsis thalia
41	67.5	19.9	466	21	AAG17437	Arabiopsis thalia
42	67.5	19.9	466	21	AAG21850	Arabiopsis thalia
43	67.5	19.9	489	21	AAG17436	Arabiopsis thalia
44	67.5	19.9	497	21	AAG21849	Arabiopsis thalia
45	67.5	19.9	844	21	AAG45432	Arabiopsis thalia

ALIGNMENTS

RESULT 1
AA192351
ID AA192351 standard; Protein; 180 AA.
XX
AC AA192351;
XX
DT 10-AUG-2000 (first entry)
XX
DE Human vasostatin (calreticulin N-terminal 180 amino acids).
XX
KW MBP-calreticulin; maltose binding protein; vasostatin; N-terminal;
KW angiogenesis; inhibition; endothelial cell; anti-angiogenic;
KW neuroprotective; antidiabetic; cytostatic; dermatological; hepatic;
KW immunosuppressive; antiinflammatory; anti-atherosclerotic;
KW gastrointestinal; anti-arthritis; ophthalmic.
XX
OS Homo sapiens.
XX
OS Synthetic.
XX
PN WO200020577-A1.
XX
PD 13-APR-2000.
XX
PF 05-OCT-1999; 99WO-US23240.
XX
PR 06-OCT-1998; 98US-0103438.
XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Tosato G, Pike SE, Yao L;
XX
DR WPI; 2000-303767/26.
XX
PT Inhibiting endothelial cell growth and angiogenesis using calreticulin,

PT useful for suppressing tumor growth
XX Claim 4; Page 82; 99pp; English.
XX A novel method of inhibiting endothelial cell growth comprises
CC contacting the cells with calreticulin (or its fragments/variants).
CC Fragments of calreticulin causes at least 40% inhibition of angiogenesis,
CC tumor growth and/or endothelial cell growth (claimed). The method may be
CC used for inhibiting angiogenesis in a patient. The angiogenesis is
CC associated with a disease other than a tumor that is associated with
CC neovascularization (e.g. diabetic neuropathy, retrolental fibroplasia,
CC trachoma, neovascular glaucoma, psoriasis, angiofibromas, immune
CC inflammation, atherosclerosis, excessive wound repair, retinal
CC neovascularization, macular degeneration, corneal graft rejection,
CC contact lens overwear, Crohn's disease, non-immune inflammation,
CC rheumatoid arthritis, systemic lupus erythematosus, thyroiditis,
CC Goodpasture's syndrome, systemic vasculitis, scleroderma, Sjorgen's
CC syndrome, sarcoidosis and primary biliary cirrhosis). The method may
CC also be used for treating/inhibiting tumor growth especially
CC Kaposi's sarcoma (claimed).
XX Sequence 180 AA;
SQ

Query Match 100.0%; Score 340; DB 21; Length 180;
Best Local Similarity 100.0%; Pred. No. 4.3e-39;
Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TDMHGEYNIMFGPDICGPGTKKHVIVNYKGNVLINKDKDDETHLYTLVRPD 60
|||||
DB 103 tdmhgdeynimfgpdicgpgtkkhvifnykgknlkdkckddefthlytlvrpd 162

QY 61 N 61
DB 163 n 163

RESULT 2
AAP92350
ID AAP92350 standard; Protein; 400 AA.
XX
AC AAP92350;
XX
DT 10-AUG-2000 (first entry)
XX
DE Recombinant human MBP-calreticulin.
XX
KW MBP-calreticulin; maltose binding protein; angiogenesis; inhibition;
KW endothelial cell; anti-angiogenic; neuroprotective; antidiabetic;
KW cytostatic; dermatologic; immunosuppressive; antiinflammatory; hepatic;
KW anti-atherosclerotic; gastrointestinal; anti-arthritis; ophthalmic.
XX
OS Homo sapiens.
XX
PN WO200020577-A1.
XX
PD 13-APR-2000.
XX
PF 05-OCT-1999; 99WO-US23240.
XX
PR 06-OCT-1998; 98US-0103438.
XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Tosato G, Pike SE, Yao L;
XX
XX WPI; 2000-303767/26.
DR N-PSDB; AAA09346, AAA09347.
XX
XX Inhibiting endothelial cell growth and angiogenesis using calreticulin,
PT useful for suppressing tumor growth
XX Claim 4; Page 80-81; 99pp; English.

Recombinant human MBP-calreticulin comprises the sequence of human
calreticulin (see AAY92349) without the 17 N-terminal amino acids.
A novel method of inhibiting endothelial cell growth comprises
contacting the cells with calreticulin (or its fragments/variants).
Fragments of calreticulin causes at least 40% inhibition of
angiogenesis, tumor growth and/or endothelial cell growth (claimed). The
method may be used for inhibiting angiogenesis in a patient. The
angiogenesis is associated with a disease other than a tumor that is
associated with neovascularization (e.g. diabetic neuropathy, retrolental
fibroplasia, trachoma, neovascular glaucoma, psoriasis, angiofibromas,
immune inflammation, atherosclerosis, excessive wound repair, retinal
neovascularization, macular degeneration, corneal graft rejection,
contact lens overwear, Crohn's disease, non-immune inflammation,
rheumatoid arthritis, systemic lupus erythematosus, thyroiditis,
Goodpasture's syndrome, systemic vasculitis, scleroderma, Sjorgen's
syndrome, sarcoidosis and primary biliary cirrhosis). The method may
also be used for treating/inhibiting tumor growth especially
Kaposi's sarcoma (claimed).
XX Sequence 400 AA;
SQ

Query Match 100.0%; Score 340; DB 21; Length 400;
Best Local Similarity 100.0%; Pred. No. 1.2e-38;
Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TDMHGEYNIMFGPDICGPGTKKHVIVNYKGNVLINKDKDDETHLYTLVRPD 60
|||||
DB 103 tdmhgdeynimfgpdicgpgtkkhvifnykgknlkdkckddefthlytlvrpd 162

QY 61 N 61
DB 163 n 163

RESULT 3
AAP92276
ID AAP92276 standard; protein; 417 AA.
XX
AC AAP92276;
XX
DT 23-FEB-1990 (first entry)
XX
DE 60 kD Ro (Ro/SSA) antigen.
XX
KW Sjorens syndrome; systemic lupus erythematosus.
XX
OS Synthetic.
XX
PN WO8909273-A.
XX
PD 05-OCT-1989.
XX
PF 22-MAR-1989; 89WO-US01213.
XX
PR 22-MAR-1988; 88US-0171634.
XX
PA (TEXA) UNIV OF TEXAS SYST.
XX
PI Sontheimer RD, Capra JD, McCauliffe DP;
XX
XX WPI; 1989-309537/42.
DR N-PSDB; AAP92276.
XX
XX DNA sequences encoding antigenic epitope(s) of Ro 60 kD autoantigen
- used in immunoassays to detect rheumatic disease
XX Disclosure; Fig 2; 88pp; English.
XX Synthetic peptides corresp. to an epitopic core of Ro antigen are
CC expressed recombinantly to detect autoantibodies, for identification
CC of autoimmune diseases. These epitopes are AAs 24-36, 23-36, 188-209,
CC

CC or 241-255. The peptides may be substd. for ribonucleoprotein particle
 CC antigens.

XX Sequence 417 AA;

Query Match 100.0%; Score 340; DB 10; Length 417;
 Best Local Similarity 100.0%; Pred. No. 1.2e-38;
 Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TDMHGDSEYNIMFGPDICGPGTKKVVHVFNYKGNVLINKDIRCKDDETHLYTLIVRPD 60
 |||||
 Db 120 tdmhgdseynimfgpdicpggkckkvhvfnykgnvlinkdirckddefthlytlivrp 179

QY 61 N 61

Db 180 n 180

RESULT 4

AA00927
 ID AAY00927 standard; Protein; 417 AA.

XX

AC AAY00927;

XX 28-MAY-1999 (first entry)

XX Calreticulin.

XX Clq and collectin receptor; cClqR binding domain; complement ubiquitin;
 KW CUB functionality; inhibitor; complement activation; inflammation;
 KW myocardial infarction; brain ischaemia; gut ischaemia; amyloid plaque;
 KW rheumatoid arthritis; systemic lupus erythematosus; Alzheimer's disease;
 KW immune complex nephritis; therapy.

XX Homo sapiens.

XX WO9907406-A1.

XX 18-FEB-1999.

PF 12-AUG-1998; 98WO-GB02430.

PR 12-AUG-1997; 97GB-0016998.

XX (UYLE-) UNIV LEICESTER.

XX Schwaebler W;

XX WPI; 1999-180404/15.

XX Use of a cClqR binding domain - to modulate complement ubiquitin
 (CUB) functionality.

XX Disclosure; Page 26-27; 31pp; English.

XX This sequence is calreticulin, a homologue of Clq and collectin receptor
 (cClqR). The invention relates to the use of a cClqR binding domain in a
 CC medicament to effect complement ubiquitin (CUB) functionality, and an
 CC inhibitor of the cClqR binding domain in a medicament to inhibit CUB
 CC functionality. The cClqR binding domain, or its inhibitor, can be used to
 CC treat a human or animal body. Particularly an inhibitor is used to treat
 CC complement activation involved in the initiation and maintenance of
 CC inflammation, for example in myocardial infarction, brain ischaemia
 CC (stroke), gut ischaemia, rheumatoid arthritis, systemic lupus
 CC erythematosus, burns, immune complex nephritis, and to treat amyloid
 CC plaques in Alzheimer's disease. The use of cClqR binding domain or
 CC inhibitor enables the CUB domain functionality to be modulated using a
 CC low molecular weight molecule.

XX Sequence 417 AA;

Query Match 100.0%; Score 340; DB 20; Length 417;
 Best Local Similarity 100.0%; Pred. No. 1.2e-38;
 Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TDMHGDSEYNIMFGPDICGPGTKKVVHVFNYKGNVLINKDIRCKDDETHLYTLIVRPD 60
 |||||
 Db 120 tdmhgdseynimfgpdicpggkckkvhvfnykgnvlinkdirckddefthlytlivrp 179

QY 61 N 61

Db 180 n 180

RESULT 5

AA092349
 ID AAY92349 standard; Protein; 417 AA.

XX

AC AAY92349;

XX 10-AUG-2000 (first entry)

XX Human MBP-calreticulin.

XX MBP-calreticulin; maltose binding protein; angiogenesis; inhibition;
 KW endothelial cell; anti-angiogenic; neuroprotective; antidiabetic;
 KW cytostatic; dermalogical; immunosuppressive; antiinflammatory; hepatic;
 KW anti-atherosclerotic; gastrointestinal; anti-arthritis; ophthalmic.

XX Homo sapiens.

XX Key Location/Qualifiers

XX Peptide 1..17

XX FT /label= signal_peptide

XX FT 18

XX FT /label= mature_protein

XX WO200020577-A1.

XX 13-APR-2000.

XX 05-OCT-1999; 99WO-US23240.

XX 06-OCT-1998; 98US-0103438.

XX (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX Tosato G, Pike SE, Yao L;

XX WPI; 2000-303767/26.

XX N-PSDB; AAA09346, AAA09347.

XX Inhibiting endothelial cell growth and angiogenesis using calreticulin,
 useful for suppressing tumor growth

XX Disclosure; Page 79-80; 99pp; English.

XX A novel method of inhibiting endothelial cell growth comprises
 CC contacting the cells with calreticulin (or its fragments/variants).
 CC Fragments of calreticulin causes at least 40% inhibition of angiogenesis,
 CC tumor growth and/or endothelial cell growth (claimed). The method may be
 CC used for inhibiting angiogenesis in a patient. The angiogenesis is
 CC associated with a disease other than a tumor that is associated with
 CC neovascularization (e.g. diabetic neuropathy, retrolental fibroplasia,
 CC trachoma, neovascular glaucoma, psoriasis, angiodermas, immune
 CC inflammation, atherosclerosis, excessive wound repair, retinal
 CC neovascularization, macular degeneration, corneal graft rejection,
 CC contact lens overwear, Crohn's disease, non-immune inflammation,
 CC rheumatoid arthritis, systemic lupus erythematosus, thyroiditis,
 CC Goodpasture's syndrome, systemic vasculitis, scleroderma, Sjorgen's
 CC syndrome, sarcoidosis and primary biliary cirrhosis). The method may
 CC also be used for treating/inhibiting tumor growth especially
 CC Kaposi's sarcoma (claimed).

XX

SQ Sequence 417 AA;

Query Match 100.0%; Score 340; DB 21; Length 417;
 Best Local Similarity 100.0%; Pred. No. 1.2e-38;
 Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TDMHGDSEYNIMFGPDICGPGTKKVVHFNKGNVINKDIRCKDDEFTHLYTLIVRPD 60
 |||||
 Db 120 tdmhgdsynimfgpdicpgptkkvvhfnkgnvlnkldirckddefthlytlivrp 179

QY 61 N 61
 |
 Db 180 n 180

RESULT 6

AAW11156
ID AAW11156 standard; peptide; 401 AA.

XX AC AAW11156;

XX DT 31-MAY-1997 (first entry)

XX DE Calreticulin.

XX KW calreticulin; C-domain; restenosis; inhibitor.

XX OS Homo sapiens.

XX PN WO9636643-A1.

XX PD 21-NOV-1996.

XX PF 17-MAY-1996; 96WO-IB00471.

XX PR 16-MAY-1996; 96US-0649417.

XX PR 17-MAY-1995; 95US-0442844.

XX PA (UYAL-) UNIV ALBERTA.

XX PI Lucas A, Michalak M;

XX PS WPI; 1997-012036/01.

PT Inhibition of restenosis in patients - using calreticulin or a
 PT C-domain polypeptide of calreticulin or a variant with the same
 PT activity.

XX PS Disclosure; Fig 1; 48pp; English.

XX CC The present sequence is calreticulin. It and a C-domain derived peptide
 CC (AAW06736) are useful for treating a patient to inhibit restenosis. The
 CC calreticulin-type cpds. are administered either parenterally,
 CC intravenously or via a catheter and can target areas of vascular damage
 CC to inhibit or prevent restenosis.

XX SQ Sequence 401 AA;

Query Match

Best Local Similarity 98.5%; Score 335; DB 18; Length 401;
 Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DMHGDSEYNIMFGPDICGPGTKKVVHFNKGNVINKDIRCKDDEFTHLYTLIVRPD 61

|||||
 Db 104 dmhgdsynimfgpdicpgptkkvvhfnkgnvlnkldirckddefthlytlivrp 163

RESULT 7

AAW04171

ID AAW04171 standard; Protein; 403 AA.

XX

AC AAW04171;

XX DT 12-DEC-1996 (first entry)

XX DE Flea calreticulin PctCal403.

XX KW Calreticulin; flea; haematophagous insect; allergic dermatitis;

XX KW vaccine; therapy; PctCal403.

XX OS Ctenocephalides felis.

XX PN WO9628469-A1.

XX PD 19-SEP-1996.

XX PF 08-MAR-1996; 96WO-US03133.

XX PR 09-MAR-1995; 95US-0401509.

XX PA (HESK-) HESKA CORP.

XX PI Rushlow KE, Stiegler GL;

XX DR WPI; 1996-442861/44.

XX DR N-PSDB; AAT39516;

XX DR N-PSDB; AAT39517.

PT Haematophagous insect calreticulin protein - used to reduce insect
 PT infestation and desensitise patients to allergic dermatitis

XX PS Claim 5; Page 68-69; 86pp; English.

XX CC Flea calreticulin protein PctCall589 (AAW04171) is a calcium-binding
 CC protein found in the salivary glands of Ctenocephalides felis.

XX CC Its amino acid sequence was deduced from a cDNA clone (AAT39516)

XX CC obtd. from a salivary gland cDNA library. Recombinant PctCall589

XX CC can be produced in host cells transformed with a vector carrying

XX CC calreticulin nucleic acids. Calreticulin alters the blood feeding

XX CC behaviour of haematophagous insects and can be administered to an

XX CC animal to reduce infestation. It reduces calreticulin activity in

XX CC insects, so reducing the insect burden on an animal. Calreticulin

XX CC can be used to elicit an immune response, thereby desensitising an

XX CC animal to allergic dermatitis caused by fleas, mosquitoes or

XX CC Culicoides.

XX SQ Sequence 403 AA;

Query Match 85.3%; Score 290; DB 17; Length 403;

Best Local Similarity 83.3%; Pred. No. 9.8e-32;

Matches 50; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

QY 2 DMHGDSEYNIMFGPDICGPGTKKVVHFNKGNVINKDIRCKDDEFTHLYTLIVRPD 61
 |||||

Db 121 dmhgdsynimfgpdicpgptkkvvhfnkgnvlnkldirckddvychvylvwxp 180

RESULT 8

AAR12312

ID AAR12312 standard; Protein; 336 AA.

XX AC AAR12312;

XX DT 29-AUG-1991 (first entry)

XX DE Partial sequence of Onchocera volvulus 42 kD antigen.

XX KW River blindness; onchocerciasis; vaccine; antigen; parasite.

XX OS Onchocerca volvulus.

XX FH Key

XX FT Region 160..166

XX FT Location/Qualifiers

[illegible]

PS Claim 1; Fig 3; 45pp; English.

XX The present invention provides the protein and coding sequences for the
 CC castor bean calreticulin protein and the calreticulin promoter sequence.
 CC In addition, the castor bean calnexin protein, coding sequence and
 CC promoter are also described. Calreticulin and calnexin are calcium
 CC binding proteins found in the endoplasmic reticulum (er). The
 CC calreticulin promoter sequence can be used in vectors to promote the
 CC expression of foreign genes, particularly resistance genes, in plant
 CC cells.

XX Sequence 415 AA;

Query Match 59.4%; Score 202; DB 22; Length 415;

Best Local Similarity 60.7%; Pred. No. 1.5e-19;

Matches 34; Conservative 9; Mismatches 13; Indels 0; Gaps 0;

QY 5 GDSYNNIMFGPDICGPTKKVHIFNYKGNVLINKDIRCKDDEFTHLYTLIVRPD 60

Db 125 gdtpsimfgpdicgstkkvhailnyndtnhlikkevpcetdqlthvylvirpd 180

RESULT 13

AAB66343

ID AAB66343 standard; Protein; 415 AA.

XX AAB66343;

DT 05-APR-2001 (first entry)

DE Castor bean calreticulin.

KW Castor bean; calreticulin; calcium binding; er; endoplasmic reticulum;
 KW calnexin; promoter; resistance.

XX Ricinus communis.

XX US6171864-B1.

PD 09-JAN-2001.

PF 05-JUL-1996; 96US-0675816.

PR 05-JUL-1996; 96US-0675816.

PA (PION-) PIONEER HI-BRED INT INC.

XX Coughlan SJ, Winfrey RJ;

DR WPI; 2001-122335/13.

XX N-PSDB; AAF29755.

PT New nucleic acid molecules encoding a calcium binding chaperone protein
 PT in endoplasmic reticulum, calreticulin, and calreticulin promoter
 PT sequences, useful for producing foreign gene products in plant cells -

PS Disclosure; Fig 1B; 45pp; English.

XX The present invention provides the protein and coding sequences for the
 CC castor bean calreticulin protein and the calreticulin promoter sequence.
 CC In addition, the castor bean calnexin protein, coding sequence and
 CC promoter are also described. Calreticulin and calnexin are calcium
 CC binding proteins found in the endoplasmic reticulum (er). The
 CC calreticulin promoter sequence can be used in vectors to promote the
 CC expression of foreign genes, particularly resistance genes, in plant
 CC cells.

XX Sequence 415 AA;

Query Match 59.4%; Score 202; DB 22; Length 415;

Best Local Similarity 60.7%; Pred. No. 1.5e-19;

Matches 34; Conservative 9; Mismatches 13; Indels 0; Gaps 0;

QY 5 GDSYNNIMFGPDICGPTKKVHIFNYKGNVLINKDIRCKDDEFTHLYTLIVRPD 60

Db 125 gdtpsimfgpdicgstkkvhailnyndtnhlikkevpcetdqlthvylvirpd 180

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ID AAG24609 standard; Protein; 312 AA.

XX AAG24609;

DT 17-OCT-2000 (first entry)

DE Arabidopsis thaliana protein fragment SEQ ID NO: 28351.

KW Protein identification; signal transduction pathway; metabolic pathway;
 KW hybridisation assay; genetic mapping; gene expression control; promoter;
 KW termination assay.

XX Arabidopsis thaliana.

XX EP1033405-A2.

PD 06-SEP-2000.

XX 25-FEB-2000; 2000EP-0301439.

XX 25-FEB-1999; 99US-0121825.

PR 05-MAR-1999; 99US-0123180.

PR 09-MAR-1999; 99US-0123548.

PR 23-MAR-1999; 99US-0125788.

PR 25-MAR-1999; 99US-0126264.

PR 29-MAR-1999; 99US-0126785.

PR 01-APR-1999; 99US-0127462.

PR 06-APR-1999; 99US-0128234.

PR 08-APR-1999; 99US-0128714.

PR 16-APR-1999; 99US-0129845.

PR 19-APR-1999; 99US-0130077.

PR 21-APR-1999; 99US-0130449.

PR 23-APR-1999; 99US-0130510.

PR 23-APR-1999; 99US-0130891.

PR 28-APR-1999; 99US-0131449.

PR 30-APR-1999; 99US-0132048.

PR 30-APR-1999; 99US-0132407.

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PR 05-MAY-1999; 99US-0132485.

PR 06-MAY-1999; 99US-0132486.

PR 06-MAY-1999; 99US-0132487.

PR 07-MAY-1999; 99US-0132863.

PR 11-MAY-1999; 99US-0134256.

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PR 14-MAY-1999; 99US-0134219.

PR 14-MAY-1999; 99US-0134221.

PR 14-MAY-1999; 99US-0134370.

PR 18-MAY-1999; 99US-0134768.

PR 19-MAY-1999; 99US-0134941.

PR 20-MAY-1999; 99US-0135124.

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PR 27-MAY-1999; 99US-0136392.

PR 28-MAY-1999; 99US-0136782.

PR 01-JUN-1999; 99US-0137222.

PR 03-JUN-1999; 99US-0137528.

PR 04-JUN-1999; 99US-0137502.

PR 07-JUN-1999; 99US-0137724.

PR 08-JUN-1999; 99US-0138094.

PR 10-JUN-1999; 99US-0138540.

PR 10-JUN-1999; 99US-0138847.

PR 14-JUN-1999; 99US-0139119.

PR 16-JUN-1999; 99US-0139452.

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ID AAG47933 standard; Protein; 312 AA.
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AC AAG47933;
XX
DT 18-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana protein fragment SEQ ID NO: 60470.
XX
KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
XX
OS Arabidopsis thaliana.
XX
PN EP1033405-A2.
XX
PD 06-SEP-2000.
XX
PF 25-FEB-2000; 2000EP-0301439.
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PR 06-MAY-1999; 99US-0132486.
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PR 07-JUN-1999; 99US-0137724.
PR 08-JUN-1999; 99US-0138094.
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PR 06-JUL-1999; 99US-0142390.
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PR 14-JUL-1999; 99US-0143624.
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PR 10-AUG-1999; 99US-0148171.
PR 11-AUG-1999; 99US-0148319.
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PR 16-AUG-1999; 99US-0149368.
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PR 18-AUG-1999; 99US-0149426.
PR 20-AUG-1999; 99US-0149722.
PR 20-AUG-1999; 99US-0149723.

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35,803 Million cell updates/sec

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Searched: 212252 seqs, 22503292 residues

Total number of hits satisfying chosen parameters: 212252

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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37	53	15.6	325	1	US-08-454-097-8	Sequence 8, Appl
38	53	15.6	325	1	US-08-453-866-8	Sequence 8, Appl
39	53	15.6	325	3	US-08-185-359-8	Sequence 8, Appl
40	53	15.6	337	1	US-08-447-500-10	Sequence 10, Appl
41	53	15.6	337	1	US-08-454-097-12	Sequence 12, Appl
42	53	15.6	337	1	US-08-453-866-10	Sequence 10, Appl
43	53	15.6	337	3	US-09-100-664A-11	Sequence 11, Appl
44	53	15.6	337	3	US-09-100-664A-12	Sequence 12, Appl
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ALIGNMENTS

RESULT 1
US-08-675-816-2
; Sequence 2, Application US/08675816
; Patent No. 6171864
; GENERAL INFORMATION:
; APPLICANT: Coughlan, Sean J.
; APPLICANT: Winfrey, Jr., Ron J.
; TITLE OF INVENTION: CALRETICULIN AND CALNEXIN GENES AND PROMOTER REGIONS AND US
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed and Berry
; STREET: 701 Fifth Ave. Suite 6300
; CITY: Seattle
; STATE: Washington
; COUNTRY: U.S.A.
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/675,816
; FILING DATE: 05-JUL-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 6171864tenburg, Carol
; REGISTRATION NUMBER: 39,317
; REFERENCE/DOCKET NUMBER: 750027.401
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206-622-4900
; TELEFAX: (206)-682-6031
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 415 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-675-816-2

Query Match 59.4%; Score 202; DB 4; Length 415;
Best Local Similarity 60.7%; Pred. No. 3.7e-19;
Matches 34; Conservative 9; Mismatches 13; Indels 0; Gaps 0;

QY 5 GDSEYNMFGPDICGPTKKVHVIFNYKGNVLINKDIRCKDDEFTHLYTLVIRPD 60

Db 125 GDTPTSIMFGPDICGPTKKVHVIFNYKGNVLINKDIRCKDDEFTHLYTLVIRPD 180

RESULT 2
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; Sequence 6, Application US/08675816
; Patent No. 6171864
; GENERAL INFORMATION:
; APPLICANT: Coughlan, Sean J.
; APPLICANT: Winfrey, Jr., Ron J.
; TITLE OF INVENTION: CALRETICULIN AND CALNEXIN GENES AND PROMOTER REGIONS AND USES
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed and Berry
; STREET: 701 Fifth Ave. Suite 6300
; CITY: Seattle
; STATE: Washington
; COUNTRY: U.S.A.
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/675,816
; FILING DATE: 05-JUL-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 6171864tenburg, Carol
; REGISTRATION NUMBER: 39,317
; REFERENCE/DOCKET NUMBER: 750027.401
; TELEPHONE: (206)-682-4900
; TELEFAX: (206)-682-6031
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 542 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-675-816-6

Query Match 36.9%; Score 125.5; DB 4; Length 542;
Best Local Similarity 42.4%; Pred. No. 9.7e-09;
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QY 56 IVRPDN 61
Db 190 ILKPDN 195

RESULT 3
US-08-296-362-2
; Sequence 2, Application US/08296362
; Patent No. 5691306
; GENERAL INFORMATION:
; APPLICANT: Bergeron, John J.M.
; APPLICANT: Thomas, David Y.
; APPLICANT: Wada, Ikuo
; TITLE OF INVENTION: METHODS OF DETECTION AND TREATMENT OF
; TITLE OF INVENTION: PROTEIN TRAFFICKING DISORDERS AND INCREASING SECRETORY
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED AND BERRY
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98104-7092

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/296,362
; FILING DATE: 25-AUG-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Deehr, Manya S.
; REGISTRATION NUMBER: 37,120
; REFERENCE/DOCKET NUMBER: 690066.401C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; TELEX: 3723836
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 593 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-296-362-2
Query Match 35.4%; Score 120.5; DB 1; Length 593;
Best Local Similarity 39.7%; Pred. No. 5.1e-08;
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QY 54 TLIVRPDN 61
Db 240 TLILNPDN 247
RESULT 4
US-08-378-761A-78
; Sequence 78, Application US/08378761A
; Patent No. 5635384
; GENERAL INFORMATION:
; APPLICANT: WALSH, TERENCE A
; APPLICANT: HEY, TIMOTHY D
; APPLICANT: MORGAN, ALICE ER
; TITLE OF INVENTION: RIBOSOME-INACTIVATING PROTEINS, INACTIVE
; TITLE OF INVENTION: PRECURSOR FORMS THEREOF, A PROCESS FOR MAKING A METHOD OF
; TITLE OF INVENTION: USING
; NUMBER OF SEQUENCES: 81
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ANDREA T. BORUCKI
; STREET: 9330 ZIONSVILLE ROAD
; CITY: INDIANAPOLIS
; STATE: IN
; COUNTRY: US
; ZIP: 46268
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/378,761A
; FILING DATE: 26-JAN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: BORUCKI, ANDREA T
; REGISTRATION NUMBER: 33651
; REFERENCE/DOCKET NUMBER: 38272B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (317) 337-4846


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; TITLE OF INVENTION: Preparation and Use for Ribosome-Inactivating Proteins
; NUMBER OF SEQUENCES: 101
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; ADDRESSEE: Bicknell
; STREET: Two First National Plaza, 20 South Clark
; STREET: Street
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60603
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/988,430
; FILING DATE: 19921209
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/901,707
; FILING DATE: 19-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/787,567
; FILING DATE: 04-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5416202and, Greta E.
; REGISTRATION NUMBER: 35302
; REFERENCE/DOCKET NUMBER: 31133
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 346-5750
; TELEFAX: (312) 984-9740
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 7:
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; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; UN-07-988-430-7

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Matches 14; Conservative 10; Mismatches 16; Indels 8; Gaps 2;

QY 9 YNI-MFGPDICGPTKKVHVFNYKGNVLINKDIRCKDDEFTHLYTL 55
||| : | : | : | : | : | : | : | : | : | : | : | : | :
Db 32 YNIPLLLPSVSGAGRYLLMHLFNYDGKTTTVAADV-----TNNVIM 72

RESULT 8
US-08-425-336-7
; Sequence 7, Application US/08425336
; Patent No. 5621083
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; APPLICANT: Carroll, Stephen F.
; APPLICANT: Studnika, Gary M.
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
; TITLE OF INVENTION: Proteins
; NUMBER OF SEQUENCES: 140
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

; TITLE OF INVENTION: Preparation and Use for Ribosome-Inactivating Proteins
; NUMBER OF SEQUENCES: 101
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; ADDRESSEE: Bicknell
; STREET: Two First National Plaza, 20 South Clark
; STREET: Street
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60603
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/988,430
; FILING DATE: 19921209
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/901,707
; FILING DATE: 19-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/787,567
; FILING DATE: 04-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Meyers, Thomas C.
; REGISTRATION NUMBER: P-36,989
; REFERENCE/DOCKET NUMBER: 31394
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6300
; TELEFAX: 312/474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 263 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-425-336-7

Query Match 17.1%; Score 58; DB 1; Length 263;
Best Local Similarity 29.2%; Pred. No. 4.5;
Matches 14; Conservative 10; Mismatches 16; Indels 8; Gaps 2;

QY 9 YNI-MFGPDICGPTKKVHVFNYKGNVLINKDIRCKDDEFTHLYTL 55
||| : | : | : | : | : | : | : | : | : | : | : | : | :
Db 32 YNIPLLLPSVSGAGRYLLMHLFNYDGKTTTVAADV-----TNNVIM 72

RESULT 9
US-08-488-113B-7
; Sequence 7, Application US/08488113B
; Patent No. 5744580
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; APPLICANT: Carroll, Stephen F.
; APPLICANT: Studnika, Gary M.
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
; TITLE OF INVENTION: Proteins
; NUMBER OF SEQUENCES: 169
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
; STREET: 500 West Madison Street, 34th floor
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60661
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/488,113B
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/425,336
; FILING DATE: 18-APR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/064,691
; FILING DATE: 12-MAY-1993
```


;; PRIOR APPLICATION DATA: US 07/988,430
;; APPLICATION NUMBER: US 07/988,430
;; FILING DATE: 09-DEC-1992
;; PRIOR APPLICATION DATA: US 07/901,707
;; APPLICATION NUMBER: US 07/901,707
;; FILING DATE: 19-JUN-1992
;; PRIOR APPLICATION DATA: US 07/787,567
;; APPLICATION NUMBER: US 07/787,567
;; FILING DATE: 04-NOV-1991
;; ATTORNEY/AGENT INFORMATION:
;; NAME: McNicholas, Janet M.
;; REGISTRATION NUMBER: 32,918
;; REFERENCE/DOCKET NUMBER: 11022US07/200-70.P3.C2A
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 312/707-9155
;; TELEFAX: 312/707-9155
;; TELEX: 650 388-1248
;; INFORMATION FOR SEQ ID NO: 7:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 263 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
US-08-488-113B-7

Query Match 17.1%; Score 58; DB 1; Length 263;
Best Local Similarity 29.2%; Pred. No. 4.5;
Matches 14; Conservative 10; Mismatches 16; Indels 8; Gaps 2;

QY 9 YNI-MFGPDICGPTKKVHVIFNYKGNVLINKDIRCKDDETHLYTL 55
||| : | : | : | : | : | : | : | : | : | : | : | : | :
Db 32 YNIPLLPSVSGAGRYLLHFLNFDYDKTITVAADV-----TNNYIM 72

RESULT 10
US-08-477-484B-7
; Sequence 7, Application US/08477484B
; Patent No. 5756699
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; APPLICANT: Carroll, Stephen F.
; APPLICANT: Studnika, Gary M.
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
; TITLE OF INVENTION: Proteins
; NUMBER OF SEQUENCES: 169
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
; STREET: 500 West Madison Street, 34th floor
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60661
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/477,484B
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/425,336
; FILING DATE: 18-APR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/064,691
; FILING DATE: 12-MAY-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/988,430
; FILING DATE: 09-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/901,707

;; FILING DATE: 19-JUN-1992
;; PRIOR APPLICATION DATA: US 07/787,567
;; APPLICATION NUMBER: US 07/787,567
;; FILING DATE: 04-NOV-1991
;; ATTORNEY/AGENT INFORMATION:
;; NAME: McNicholas, Janet M.
;; REGISTRATION NUMBER: 32,918
;; REFERENCE/DOCKET NUMBER: 11022US07/200-70.P3.C2A
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 312/707-9155
;; TELEFAX: 312/707-9155
;; TELEX: 650 388-1248
;; INFORMATION FOR SEQ ID NO: 7:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 263 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
US-08-477-484B-7

Query Match 17.1%; Score 58; DB 1; Length 263;
Best Local Similarity 29.2%; Pred. No. 4.5;
Matches 14; Conservative 10; Mismatches 16; Indels 8; Gaps 2;

QY 9 YNI-MFGPDICGPTKKVHVIFNYKGNVLINKDIRCKDDETHLYTL 55
||| : | : | : | : | : | : | : | : | : | : | : | : | :
Db 32 YNIPLLPSVSGAGRYLLHFLNFDYDKTITVAADV-----TNNYIM 72

RESULT 11
US-08-646-360-7
; Sequence 7, Application US/08646360
; Patent No. 5837491
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; APPLICANT: Carroll, Stephen F.
; APPLICANT: Studnika, Gary M.
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
; TITLE OF INVENTION: Proteins
; NUMBER OF SEQUENCES: 173
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
; STREET: 500 West Madison Street, 34th floor
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60661
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/646,360
; FILING DATE: 13-MAY-1996
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/05348
; FILING DATE: 12-MAY-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/064,691
; FILING DATE: 12-MAY-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/988,430
; FILING DATE: 09-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/901,707
; FILING DATE: 19-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/787,567
; FILING DATE: 04-NOV-1991
; ATTORNEY/AGENT INFORMATION:

TELEPHONE: 312/707-8889

SEQUENCE CHARACTERISTICS:
LENGTH: 263 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-136-389-7

Query Match 17.1%; Score 58; DB 4; Length 263;
Best Local Similarity 29.2%; Pred. No. 4.5;
Matches 14; Conservative 10; Mismatches 16; Indels 8; Gaps 2;

Qy 9 YNI-MFGPDICGPGTKVHVIFNYKGNVLINKDKRCKDDETHLYTL 55
||| : | : | : ||| : | : | : | : | : | : | : | : | : | :
Db 32 YNIPLLPSVSGAGRYLLMHLFNYDGKTTITVADV-----TNYIM 72

RESULT 14

PCT-US92-09487-7
Sequence 7, Application PC/TUS9209487
GENERAL INFORMATION:
APPLICANT: Bernhard, Susan L.
APPLICANT: Better, Marc D.
APPLICANT: Carroll, Stephen F.
APPLICANT: Lane, Julie A.
APPLICANT: Lei, Shau-Ping
TITLE OF INVENTION: Materials Comprising and Methods of
TITLE OF INVENTION: Preparation and Use for Ribosome-Inactivating Proteins
NUMBER OF SEQUENCES: 101
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
ADDRESSEE: Bicknell
STREET: Two First National Plaza, 20 South Clark
STREET: Street
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60603
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/09487
FILING DATE: 19921104
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: Noland, Greta E.
REGISTRATION NUMBER: 35302
REFERENCE/DOCKET NUMBER: 31133
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 346-5750
TELEFAX: (312) 984-9740
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 263 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US92-09487-7

Query Match 17.1%; Score 58; DB 5; Length 263;
Best Local Similarity 29.2%; Pred. No. 4.5;
Matches 14; Conservative 10; Mismatches 16; Indels 8; Gaps 2;

Qy 9 YNI-MFGPDICGPGTKVHVIFNYKGNVLINKDKRCKDDETHLYTL 55
||| : | : | : ||| : | : | : | : | : | : | : | : | : | :
Db 32 YNIPLLPSVSGAGRYLLMHLFNYDGKTTITVADV-----TNYIM 72

RESULT 15

US-09-100-664A-10
Sequence 10, Application US/09100664A
Patent No. 6057129
GENERAL INFORMATION:
APPLICANT: YOUNG, MICHAEL W.
APPLICANT: KLOSS, BRIAN
APPLICANT: BLAU, JUSTIN
APPLICANT: PRICE, JEFFREY
TITLE OF INVENTION: A NOVEL CLOCK GENE AND METHODS OF USE
TITLE OF INVENTION: THEREOF
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue, 4th Floor
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/100,664A
FILING DATE: 19-JUN-1998
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-221
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
TELEFAX: 201-343-1684
TELEX: 133521
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 319 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
US-09-100-664A-10

Query Match 16.5%; Score 56; DB 3; Length 319;
Best Local Similarity 29.7%; Pred. No. 11;
Matches 19; Conservative 10; Mismatches 23; Indels 12; Gaps 4;

Qy 6 DSEYNIMEGPDICGPGTKVHVIFNYKGNVLINKDKRCKDDETHLYTL 57
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Db 74 EGDYNNMV-IDLIGPSLED---LFNYCNKRLSLKTVMLADOLINVEFMHTRGFLH 129

Qy 58 RPDN 61
: : : :
Db 130 KPDN 133

Search completed: January 9, 2002, 14:59:43
Job time: 70 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: January 9, 2002, 14:59:43 ; Search time 38.34 Seconds
(without alignments)
15.847 Million cell updates/sec

Title: US-09-828-000-5
Perfect score: 151
Sequence: 1 CGPGTKKHVIFNYKGNVINKDIRC 27
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 212252 seqs, 22503292 residues

Total number of hits satisfying chosen parameters: 212252

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA.*
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2: /cgn2_6/ptodata/2/1aa/5B-COMB.pap.*
3: /cgn2_6/ptodata/2/1aa/6A-COMB.pap.*
4: /cgn2_6/ptodata/2/1aa/6B-COMB.pap.*
5: /cgn2_6/ptodata/2/1aa/PCFUS-COMB.pap.*
6: /cgn2_6/ptodata/2/1aa/backfiles.pap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	82	54.3	415	4	US-08-675-816-2
2	49	32.5	593	1	US-08-208-036-17
3	49	32.5	593	1	US-08-428-823-17
4	49	32.5	876	2	US-08-633-476-2
5	49	32.5	877	1	US-08-208-036-14
6	49	32.5	877	1	US-08-428-823-14
7	48	31.8	17	4	US-08-996-679-63
8	48	31.8	17	4	US-08-939-833A-14
9	48	31.8	17	4	US-09-113-395-23
10	48	31.8	17	4	US-09-113-977C-68
11	47	31.1	490	1	US-08-361-611-2
12	47	31.1	490	1	US-08-565-655-2
13	47	31.1	490	2	US-08-946-987-2
14	44.5	29.5	149	3	US-08-836-236-9
15	44	29.1	113	4	US-08-975-762-67
16	44	29.1	113	4	US-09-295-028-67
17	44	29.1	113	4	US-09-106-582-67
18	44	29.1	496	4	US-08-924-183-10
19	44	29.1	496	4	US-09-488-364-10
20	43.5	28.8	351	1	US-08-415-751-18
21	43	28.5	76	2	US-08-117-952-757
22	43	28.5	250	1	US-08-378-761A-78
23	43	28.5	250	1	US-08-485-286-78
24	43	28.5	263	1	US-07-901-707-7
25	43	28.5	263	1	US-07-988-430-7
26	43	28.5	263	1	US-08-425-336-7
27	43	28.5	263	1	US-08-488-113B-7

28	43	28.5	263	1	US-08-477-484B-7	Sequence 7, Appli
29	43	28.5	263	2	US-08-646-360-7	Sequence 7, Appli
30	43	28.5	263	4	US-08-839-765-7	Sequence 7, Appli
31	43	28.5	263	4	US-09-136-389-7	Sequence 7, Appli
32	43	28.5	263	5	PCT-US92-09487-7	Sequence 7, Appli
33	42	27.8	499	2	US-09-032-315-3	Sequence 3, Appli
34	42	27.8	499	2	US-08-993-318A-3	Sequence 3, Appli
35	42	27.8	499	4	US-09-399-886-3	Sequence 3, Appli
36	42	27.8	499	4	US-09-396-260-3	Sequence 3, Appli
37	42	27.8	499	4	US-09-576-281-3	Sequence 3, Appli
38	42	27.8	510	2	US-08-300-584-4	Sequence 4, Appli
39	42	27.8	510	4	US-08-476-123-4	Sequence 4, Appli
40	42	27.8	519	1	US-08-462-484-4	Sequence 4, Appli
41	42	27.8	519	1	US-08-441-147-4	Sequence 4, Appli
42	42	27.8	519	5	PCT-US95-07536-4	Sequence 4, Appli
43	42	27.8	590	4	US-08-743-168B-43	Sequence 43, Appli
44	42	27.8	911	1	US-08-596-985-2	Sequence 2, Appli
45	41	27.2	503	2	US-08-481-337A-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1
US-08-675-816-2
; Sequence 2, Application US/08675816
; Patent No. 6171864
; GENERAL INFORMATION:
; APPLICANT: Coughlan, Sean J.
; APPLICANT: Winfrey, Jr., Ron J.
; TITLE OF INVENTION: CALRETICULIN AND CALNEXIN GENES AND PROMOTER REGIONS AND US
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed and Berry
; STREET: 701 Fifth Ave. Suite 6300
; CITY: Seattle
; STATE: Washington
; COUNTRY: U.S.A.
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/675,816
; FILING DATE: 05-JUL-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 6171864tenburg, Carol
; REGISTRATION NUMBER: 39,317
; REFERENCE/DOCKET NUMBER: 750027.401
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206-622-4900
; TELEFAX: (206)-682-6031
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 415 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-675-816-2

Query Match 54.3%; Score 82; DB 4; Length 415;
Best Local Similarity 55.6%; Pred. No. 0.00013;
Matches 15; Conservative 2; Mismatches 10; Indels 0; Gaps 0;

Qy 1 CGPGTKKHVIFNYKGNVINKDIRC 27
||| ||||| ||| ||| ||| |||

Db 138 CGYSTKKVHAILNYNDTNHLIKKEVPC 164

RESULT 2
US-08-208-036-17
; Sequence 17, Application US/08208036
; Patent No. 5436326
; GENERAL INFORMATION:
; APPLICANT: Yoshizumi ISHINO et al.
; TITLE OF INVENTION: METHOD FOR CLONING OF A GENE FOR POL I TYPE
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Wenderoth, Lind & Ponack
; STREET: 805 Fifteenth Street, N.W., #700
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 500 kb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: DisplayWrite
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/208,036
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION NUMBER: US/07/887,282
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Warren M. Cheek, Jr.
; REGISTRATION NUMBER: 33,367
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-8850
; TELEFAX:
; TELEX:
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 593 amino acid residues
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL:
; ANTI-SENSE:
; FRAGMENT TYPE:
; ORIGINAL SOURCE:
; ORGANISM:
; STRAIN:
; INDIVIDUAL ISOLATE:
; DEVELOPMENTAL STAGE:
; HAPLOTYPE:
; TISSUE TYPE:
; CELL LINE:
; ORGANELLE:
; IMMEDIATE SOURCE:
; LIBRARY:
; CLONE:
; POSITION IN GENOME:
; CHROMOSOME/SEGMENT:
; MAP POSITION:
; UNITS:
; FEATURE:
; NAME/KEY:
; LOCATION:
; IDENTIFICATION METHOD:
; OTHER INFORMATION:
; PUBLICATION INFORMATION:
; AUTHORS:
; TITLE:
; JOURNAL:
; VOLUME:

; ISSUE:
; PAGES:
; DATE:
; DOCUMENT NUMBER:
; FILING DATE:
; PUBLICATION DATE:
; RELEVANT RESIDUES IN SEQ ID NO:
US-08-208-036-17
Query Match 32.5%; Score 49; DB 1; Length 593;
Best Local Similarity 81.8%; Pred. No. 19;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 3 PGTKKVHVIFN 13
| | | | | | | |
DB 314 PDTKKVHTIFN 324
RESULT 3
US-08-428-823-17
; Sequence 17, Application US/08428823
; Patent No. 5753482
; GENERAL INFORMATION:
; APPLICANT: Yoshizumi ISHINO et al.
; TITLE OF INVENTION: METHOD FOR CLONING OF A GENE FOR
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Wenderoth, Lind & Ponack
; STREET: 805 Fifteenth Street, N.W., #700
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WordPerfect 5.1+
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/428,823
; FILING DATE: April 25, 1995
; CLASSIFICATION: 435
; PRIOR APPLICATION NUMBER:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Matthew Jacob
; REGISTRATION NUMBER: 25,154
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-8850
; TELEFAX:
; TELEX:
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 593 amino acid residues
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL:
; ANTI-SENSE:
; FRAGMENT TYPE:
; ORIGINAL SOURCE:
; ORGANISM:
; STRAIN:
; INDIVIDUAL ISOLATE:
; DEVELOPMENTAL STAGE:
; HAPLOTYPE:
; TISSUE TYPE:
; CELL TYPE:

CELL LINE:
ORGANELLE:
IMMEDIATE SOURCE:
LIBRARY:
CLONE:
POSITION IN GENOME:
CHROMOSOME/SEGMENT:
MAP POSITION:
UNITS:
FEATURE:
NAME/KEY:
LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION:
PUBLICATION INFORMATION:
AUTHORS:
TITLE:
JOURNAL:
VOLUME:
ISSUE:
PAGES:
DATE:
DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:

Query Match 32.5%; Score 49; DB 1; Length 593;
Best Local Similarity 81.8%; Pred. No. 19;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 PGTKKVHVIFN 13
| | | | | | | |
DB 314 PDTKKVHTIFN 324

RESULT 4
US-08-633-476-2
; Sequence 2, Application US/08633476
; Patent No. 5830714
; GENERAL INFORMATION:
; APPLICANT: Swaminathan, Neela
; APPLICANT: Wilkosz, Richard K.
; APPLICANT: Muller, Reinhold
; TITLE OF INVENTION: BIOLOGICALLY ACTIVE FRAGMENT OF
; TITLE OF INVENTION: BACILLUS STEAROTHEROPHILUS DNA POLYMERASE
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/633,476
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Pochopien, Donald J.
; REGISTRATION NUMBER: 32,167
; REFERENCE/DOCKET NUMBER: 28003/32630
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6300
; TELEFAX: 312/474-0448
; TELEX: 25-3856

; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 876 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-633-476-2

Query Match 32.5%; Score 49; DB 2; Length 876;
Best Local Similarity 81.8%; Pred. No. 31;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 PGTKKVHVIFN 13
| | | | | | | |
DB 597 PDTKKVHTIFN 607

RESULT 5
US-08-208-036-14
; Sequence 14, Application US/08208036
; Patent No. 5436326
; GENERAL INFORMATION:
; APPLICANT: Yoshizumi, IISHINO et al.
; TITLE OF INVENTION: METHOD FOR CLONING OF A GENE FOR POL I TYPE
; TITLE OF INVENTION: DNA POLYMERASE
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wenderoth, Lind & Ponack
; STREET: 805 Fifteenth Street, N.W., #700
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 500 kb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: DisplayWrite
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/208,036
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/887,282
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Warren M. Cheek, Jr.
; REGISTRATION NUMBER: 33,367
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-8850
; TELEFAX:
; TELEX:
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 877 amino acid residues
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL:
; ANTI-SENSE:
; FRAGMENT TYPE:
; ORIGINAL SOURCE:
; ORGANISM:
; STRAIN:
; INDIVIDUAL ISOLATE:
; DEVELOPMENTAL STAGE:
; HAPLOTYPE:
; TISSUE TYPE:
; CELL TYPE:
; CELL LINE:

ORGANELLE:
IMMEDIATE SOURCE:
LIBRARY:
CLONE:
POSITION IN GENOME:
CHROMOSOME/SEGMENT:
MAP POSITION:
UNITS:
FEATURE:
NAME/KEY:
LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION:
PUBLICATION INFORMATION:
AUTHORS:
TITLE:
JOURNAL:
VOLUME:
ISSUE:
PAGES:
DATE:
DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:
US-08-208-036-14

Query Match 32.5%; Score 49; DB 1; Length 877;
Best Local Similarity 81.8%; Pred. No. 31;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 PGTKKVHVIFN 13
DB 598 PDKKVVHTFN 608

RESULT 6
US-08-428-823-14
Sequence 14, Application US/08428823
Patent No. 5753482
GENERAL INFORMATION:
APPLICANT: Yoshizumi ISHINO et al.
TITLE OF INVENTION: METHOD FOR CLONING OF A GENE FOR
POLYMERASE
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1+
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/428,823
FILING DATE: April 25, 1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Matthew Jacob
REGISTRATION NUMBER: 25,154
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
TELEFAX:
TELEX:

INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 877 amino acid residues
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL:
ANTI-SENSE:
FRAGMENT TYPE:
ORIGINAL SOURCE:
ORGANISM:
STRAIN:
INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE:
HAPLOTYPE:
TISSUE TYPE:
CELL TYPE:
CELL LINE:
ORGANELLE:
IMMEDIATE SOURCE:
LIBRARY:
CLONE:
POSITION IN GENOME:
CHROMOSOME/SEGMENT:
MAP POSITION:
UNITS:
FEATURE:
NAME/KEY:
LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION:
PUBLICATION INFORMATION:
AUTHORS:
TITLE:
JOURNAL:
VOLUME:
ISSUE:
PAGES:
DATE:
DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:
US-08-428-823-14

Query Match 32.5%; Score 49; DB 1; Length 877;
Best Local Similarity 81.8%; Pred. No. 31;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 PGTKKVHVIFN 13
DB 598 PDKKVVHTFN 608

RESULT 7
US-08-996-679-63
Sequence 63, Application US/08996679
Patent No. 6169071
GENERAL INFORMATION:
APPLICANT: Blaschuk, Orest W.
APPLICANT: Gour, Barbara J.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING
CELL ADHESION
NUMBER OF SEQUENCES: 63
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA: US/08/996,679
APPLICATION NUMBER: US/08/996,679
FILING DATE: 23-DEC-1997
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 100086.401C1
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 63:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-08-996-679-63

Query Match 31.8%; Score 48; DB 4; Length 17;
Best Local Similarity 43.8%; Pred. No. 0.43;
Matches 7; Conservative 7; Mismatches 2; Indels 0; Gaps 0;

QY 11 IFNYKGKVNLINKDIR 26
I: :||:|:|: ||:|
DB 1 IWKHGRDVLKDKVR 16

RESULT 8
US-08-939-853A-14
; Sequence 14, Application US/08939853A
; Patent No. 6203788
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR REGULATING
; TITLE OF INVENTION: CELL ADHESION
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/939,853A
FILING DATE: 29-SEP-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 32,391
REFERENCE/DOCKET NUMBER: 100086.402
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear

US-08-939-853A-14

Query Match 31.8%; Score 48; DB 4; Length 17;
Best Local Similarity 43.8%; Pred. No. 0.43;
Matches 7; Conservative 7; Mismatches 2; Indels 0; Gaps 0;

QY 11 IFNYKGKVNLINKDIR 26
I: :||:|:|: ||:|
DB 1 IWKHGRDVLKDKVR 16

RESULT 9
US-09-115-395-23
; Sequence 23, Application US/09115395A
; Patent No. 6207639
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NEURITE OUTGROWTH
; FILE REFERENCE: 100086.401C3
; CURRENT APPLICATION NUMBER: US/09/115,395A
; CURRENT FILING DATE: 1998-07-14
; EARLIER APPLICATION NUMBER: 08/996,679
; EARLIER FILING DATE: 1997-12-23
; EARLIER APPLICATION NUMBER: 08/893,534
; EARLIER FILING DATE: 1997-07-11
; EARLIER APPLICATION NUMBER: 60/021,612
; EARLIER FILING DATE: 1996-07-12
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 23
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Solid Phase
; OTHER INFORMATION: Synthesis
US-09-115-395-23

Query Match 31.8%; Score 48; DB 4; Length 17;
Best Local Similarity 43.8%; Pred. No. 0.43;
Matches 7; Conservative 7; Mismatches 2; Indels 0; Gaps 0;

QY 11 IFNYKGKVNLINKDIR 26
I: :||:|:|: ||:|
DB 1 IWKHGRDVLKDKVR 16

RESULT 10
US-09-113-977C-68
; Sequence 68, Application US/09113977C
; Patent No. 6277824
; GENERAL INFORMATION:
; APPLICANT: Doherty, Patrick
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING ADHESION MOLECULE
; TITLE OF INVENTION: FUNCTION
; FILE REFERENCE: 100086.403
; CURRENT APPLICATION NUMBER: US/09/113,977C
; CURRENT FILING DATE: 1998-07-10
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 68
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Solid Phase
; OTHER INFORMATION: Synthesis
US-09-113-977C-68

•

Search completed: January 9, 2002, 14:59:44
Job time: 71 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: January 9, 2002, 14:59:44 ; Search time 38.34 Seconds
(without alignments)
10.565 Million cell updates/sec

Title: US-09-828-000-6
Perfect score: 96
Sequence: 1 VIFNYGKKNVLINKDIRC 18

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 212252 seqs, 22503292 residues

Total number of hits satisfying chosen parameters: 212252

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA.*
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3: /cgn2_6/ptodata/2/1aa/6A_COMB.pep.*
4: /cgn2_6/ptodata/2/1aa/6B_COMB.pep.*
5: /cgn2_6/ptodata/2/1aa/PCTUS_COMB.pep.*
6: /cgn2_6/ptodata/2/1aa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	48	50.0	17	4	US-08-996-679-63
2	48	50.0	17	4	US-08-939-853A-14
3	48	50.0	17	4	US-09-115-395-23
4	48	50.0	17	4	US-09-113-977C-68
5	44	45.8	496	4	US-08-924-183-10
6	44	45.8	496	4	US-09-488-364-10
7	43	44.8	76	2	US-08-117-952-757
8	43	44.8	415	4	US-08-675-816-2
9	41	42.7	250	1	US-08-378-761A-78
10	41	42.7	250	1	US-08-485-286-78
11	41	42.7	263	1	US-07-901-707-7
12	41	42.7	263	1	US-07-988-430-7
13	41	42.7	263	1	US-08-425-336-7
14	41	42.7	263	1	US-08-488-113B-7
15	41	42.7	263	1	US-08-477-484B-7
16	41	42.7	263	2	US-08-646-360-7
17	41	42.7	263	4	US-08-839-765-7
18	41	42.7	263	4	US-09-136-389-7
19	41	42.7	263	5	PCT-US92-09487-7
20	41	42.7	503	2	US-08-481-337A-2
21	41	42.7	503	2	US-08-696-268B-2
22	41	42.7	503	4	US-09-382-256-2
23	41	42.7	503	4	US-09-395-115-2
24	41	42.7	503	5	PCT-US94-11328A-4
25	41	42.7	503	5	PCT-US95-05467-2
26	41	42.7	581	4	US-08-743-168B-40
27	41	42.7	590	4	US-08-743-168B-43

28	40	41.7	31	4	US-08-857-076-15	Sequence 15, Appl
29	40	41.7	378	2	US-08-158-735A-11	Sequence 11, Appl
30	40	41.7	669	2	US-08-357-533A-8	Sequence 8, Appl
31	40	41.7	669	3	US-08-459-009-8	Sequence 8, Appl
32	40	41.7	669	3	US-08-459-951-8	Sequence 8, Appl
33	39	40.6	268	4	US-08-904-284-7	Sequence 7, Appl
34	39	40.6	579	4	US-08-743-168B-36	Sequence 36, Appl
35	39	40.6	777	2	US-08-231-193A-16	Sequence 16, Appl
36	39	40.6	777	2	US-08-486-273A-16	Sequence 16, Appl
37	39	40.6	777	3	US-08-480-474-16	Sequence 16, Appl
38	39	40.6	777	3	US-08-940-086A-16	Sequence 16, Appl
39	39	40.6	854	2	US-08-231-193A-32	Sequence 32, Appl
40	39	40.6	854	2	US-08-486-273A-32	Sequence 32, Appl
41	39	40.6	854	3	US-08-480-474-32	Sequence 32, Appl
42	39	40.6	854	3	US-08-940-086A-32	Sequence 32, Appl
43	39	40.6	863	4	US-08-436-332B-2	Sequence 2, Appl
44	39	40.6	870	2	US-08-231-193A-30	Sequence 30, Appl
45	39	40.6	870	2	US-08-486-273A-30	Sequence 30, Appl

ALIGNMENTS

RESULT 1
US-08-996-679-63
; Sequence 63, Application US/08996679
; Patent No. 6169071
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING
; TITLE OF INVENTION: CELL ADHESION
; NUMBER OF SEQUENCES: 63
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED AND BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/996,679
; FILING DATE: 23-DEC-1997
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Maki, Daivd J.
; REGISTRATION NUMBER: 31,392
; REFERENCE/DOCKET NUMBER: 100086.401C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 63:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
US-08-996-679-63

Query Match 50.0%; Score 48; DB 4; Length 17;
Best Local Similarity 43.8%; Pred. No. 0.072;
Matches 7; Conservative 7; Mismatches 2; Indels 0; Gaps 0;
Qy 2 IFNYGKKNVLINKDIR 17
Db 1 IWKHGRDVLKKDVR 16

RESULT 2
US-08-939-853A-14
; Sequence 14, Application US/08939853A
; Patent No. 6203788
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR REGULATING
; TITLE OF INVENTION: CELL ADHESION
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED AND BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/939,853A
; FILING DATE: 29-SEP-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Muki, David J.
; REGISTRATION NUMBER: 32,391
; REFERENCE/DOCKET NUMBER: 100086.402
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
US-08-939-853A-14

Query Match 50.0%; Score 48; DB 4; Length 17;
Best Local Similarity 43.8%; Pred. No. 0.072;
Matches 7; Conservative 7; Mismatches 2; Indels 0; Gaps 0;

QY 2 IFNYKGNVLINKDIR 17
I: :||:|:|:|:|:|:|:|:|
Db 1 IWKHGRDVLKDKVR 16

RESULT 3
US-09-115-395-23
; Sequence 23, Application US/09115395A
; Patent No. 6207639
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NEURITE OUTGROWTH
; FILE REFERENCE: 100086.401C3
; CURRENT APPLICATION NUMBER: US/09/115,395A
; CURRENT FILING DATE: 1998-07-14
; EARLIER APPLICATION NUMBER: 08/996,679
; EARLIER FILING DATE: 1997-12-23
; EARLIER APPLICATION NUMBER: 08/893,534
; EARLIER FILING DATE: 1997-07-11
; EARLIER APPLICATION NUMBER: 60/021,612
; EARLIER FILING DATE: 1996-07-12
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 23
; LENGTH: 17

; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Solid Phase
; OTHER INFORMATION: Synthesis
US-09-115-395-23

Query Match 50.0%; Score 48; DB 4; Length 17;
Best Local Similarity 43.8%; Pred. No. 0.072;
Matches 7; Conservative 7; Mismatches 2; Indels 0; Gaps 0;

QY 2 IFNYKGNVLINKDIR 17
I: :||:|:|:|:|:|:|:|:|
Db 1 IWKHGRDVLKDKVR 16

RESULT 4
US-09-113-977C-68
; Sequence 68, Application US/09113977C
; Patent No. 6277824
; GENERAL INFORMATION:
; APPLICANT: Doherty, Patrick
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING ADHESION MOLECULE
; TITLE OF INVENTION: FUNCTION
; FILE REFERENCE: 100086.403
; CURRENT APPLICATION NUMBER: US/09/113,977C
; CURRENT FILING DATE: 1998-07-10
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 68
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Solid Phase
; OTHER INFORMATION: Synthesis
US-09-113-977C-68

Query Match 50.0%; Score 48; DB 4; Length 17;
Best Local Similarity 43.8%; Pred. No. 0.072;
Matches 7; Conservative 7; Mismatches 2; Indels 0; Gaps 0;

QY 2 IFNYKGNVLINKDIR 17
I: :||:|:|:|:|:|:|:|:|
Db 1 IWKHGRDVLKDKVR 16

RESULT 5
US-08-924-183-10
; Sequence 10, Application US/08924183A
; Patent No. 6218109
; GENERAL INFORMATION:
; APPLICANT: Elledge, Stephen J.
; APPLICANT: Sanchez, Yolanda
; TITLE OF INVENTION: MAMMALIAN CHECKPOINT GENES AND PROTEINS
; FILE REFERENCE: 120541-1003
; CURRENT APPLICATION NUMBER: US/08/924,183A
; CURRENT FILING DATE: 1997-09-05
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 496
; TYPE: PRT
; ORGANISM: Schizosaccharomyces pombe
US-08-924-183-10

Query Match 45.8%; Score 44; DB 4; Length 496;
Best Local Similarity 46.7%; Pred. No. 16;

RESULT 9
US-08-378-761A-78
; Sequence 78, Application US/08378761A
; Patent NO. 5635384
; GENERAL INFORMATION:

APPLICANT: WALSH, TERENCE A
APPLICANT: HEY, TIMOTHY D
APPLICANT: MORGAN, ALICE ER
TITLE OF INVENTION: RIBOSOME-INACTIVATING PROTEINS, INACTIVE
TITLE OF INVENTION: PRECURSOR FORMS THEREOF, A PROCESS FOR MAKING A METHOD OF
TITLE OF INVENTION: USING
NUMBER OF SEQUENCES: 81
CORRESPONDENCE ADDRESS:
ADDRESSER: ANDREA T. BORUCKI
STREET: 9330 ZIONSVILLE ROAD
CITY: INDIANAPOLIS
STATE: IN
COUNTRY: US
ZIP: 46268
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/378,761A
FILING DATE: 26-JAN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: BORUCKI, ANDREA T
REGISTRATION NUMBER: 33651
REFERENCE/DOCKET NUMBER: 38272B
TELEPHONE: (317) 337-4846
INFORMATION FOR SEQ ID NO: 78
SEQUENCE CHARACTERISTICS:
LENGTH: 250 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-378-761A-78

Query Match 42.7%; Score 41; DB 1; Length 250;
Best Local Similarity 40.0%; Pred. No. 23;
Matches 6; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 2 IFNYGKKNVLINKDI 16
:|||||: : : : :
Db 52 LFNYDGKTTTVAVDV 66

RESULT 10
US-08-485-286-78
Sequence 78, Application US/08485286
Patent No. 5646026
Patent No. 5646026 5646119
GENERAL INFORMATION:
APPLICANT: WALSH, TERENCE A
APPLICANT: HEY, TIMOTHY D
APPLICANT: MORGAN, ALICE ER
TITLE OF INVENTION: RIBOSOME-INACTIVATING PROTEINS, INACTIVE
TITLE OF INVENTION: PRECURSOR FORMS THEREOF, A PROCESS FOR MAKING A METHOD OF
TITLE OF INVENTION: USING
NUMBER OF SEQUENCES: 81
CORRESPONDENCE ADDRESS:
ADDRESSER: ANDREA T. BORUCKI
STREET: 9330 ZIONSVILLE ROAD
CITY: INDIANAPOLIS
STATE: IN
COUNTRY: US
ZIP: 46268
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,286
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/378761
FILING DATE: 26-JAN-1995
ATTORNEY/AGENT INFORMATION:
NAME: BORUCKI, ANDREA T
REGISTRATION NUMBER: 33651
REFERENCE/DOCKET NUMBER: 38272B
TELEPHONE: (317) 337-4846
INFORMATION FOR SEQ ID NO: 78
SEQUENCE CHARACTERISTICS:
LENGTH: 250 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-485-286-78
Query Match 42.7%; Score 41; DB 1; Length 250;
Best Local Similarity 40.0%; Pred. No. 23;
Matches 6; Conservative 4; Mismatches 5; Indels 0; Gaps 0;
QY 2 IFNYGKKNVLINKDI 16
:|||||: : : : :
Db 52 LFNYDGKTTTVAVDV 66
RESULT 11
US-07-901-707-7
Sequence 7, Application US/07901707
Patent No. 5376546
GENERAL INFORMATION:
APPLICANT: Bernhard, Susan L.
APPLICANT: Better, Marc D.
APPLICANT: Carroll, Steve F.
APPLICANT: Lane, Julie A.
TITLE OF INVENTION: Materials Comprising and Methods of
TITLE OF INVENTION: Composition and Use for Ribosome-Inactivating Proteins
NUMBER OF SEQUENCES: 57
CORRESPONDENCE ADDRESS:
ADDRESSER: Marshall, O'Toole, Gerstein, Murray &
ADDRESS: Bicknell
STREET: Two First National Plaza, 20 South Clark
STREET: Street
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60603
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/901,707
FILING DATE: 19920619
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: No. 5376546and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 27129/30910
TELEPHONE: (312) 346-5750
TELEFAX: (312) 984-5750
TELEX: 25-3856

INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 263 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-901-707-7

Query Match 42.7%; Score 41; DB 1; Length 263;
Best Local Similarity 40.0%; Pred. No. 25;
Matches 6; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 2 IFNYGKGNVLINKDI 16
:|||||||:|:
Db 52 LFNYDGKTTTVAVDV 66

RESULT 12
US-07-988-430-7
; Sequence 7, Application US/07988430
; Patent No. 5416202
; GENERAL INFORMATION:
; APPLICANT: Bernhard, Susan L.
; APPLICANT: Better, Marc D.
; APPLICANT: Carroll, Stephen F.
; APPLICANT: Lane, Julie A.
; APPLICANT: Lei, Shau-Ping
; TITLE OF INVENTION: Materials Comprising and Methods of
; TITLE OF INVENTION: Preparation and Use for Ribosome-Inactivating Proteins
; NUMBER OF SEQUENCES: 101
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; ADDRESSEE: Bicknell
; STREET: Two First National Plaza, 20 South Clark
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60603
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/988,430
; FILING DATE: 19921209
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/901,707
; FILING DATE: 19-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/787,567
; FILING DATE: 04-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5416202and, Greta E.
; REGISTRATION NUMBER: 35302
; REFERENCE/DOCKET NUMBER: 31133
; TELEPHONE: (312) 346-5750
; TELEFAX: (312) 984-9740
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 263 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-07-988-430-7

Query Match 42.7%; Score 41; DB 1; Length 263;

Best Local Similarity 40.0%; Pred. No. 25;
Matches 6; Conservative 4; Mismatches 5; Indels 0; Gaps 0;
QY 2 IFNYGKGNVLINKDI 16
:|||||||:|:
Db 52 LFNYDGKTTTVAVDV 66

RESULT 13
US-08-425-336-7
; Sequence 7, Application US/08425336
; Patent No. 5621083
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; APPLICANT: Carroll, Stephen F.
; APPLICANT: Studnika, Gary M.
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
; TITLE OF INVENTION: Proteins
; NUMBER OF SEQUENCES: 140
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/425,336
; FILING DATE: 18-APR-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/064,691
; FILING DATE: 12-MAY-1993
; APPLICATION NUMBER: US 07/901,707
; FILING DATE: 19-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/787,567
; FILING DATE: 04-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Meyers, Thomas C.
; REGISTRATION NUMBER: P-36,989
; REFERENCE/DOCKET NUMBER: 31394
; TELEPHONE: 312/474-6300
; TELEFAX: 312/474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 263 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-425-336-7

Query Match 42.7%; Score 41; DB 1; Length 263;
Best Local Similarity 40.0%; Pred. No. 25;
Matches 6; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 2 IFNYGKGNVLINKDI 16
:|||||||:|:
Db 52 LFNYDGKTTTVAVDV 66

RESULT 14
US-08-488-113B-7
; Sequence 7, Application US/08488113B
; Patent No. 5744580

```
/
/ GENERAL INFORMATION:
/ APPLICANT: Better, Marc D.
/ APPLICANT: Carroll, Stephen F.
/ APPLICANT: Studnika, Gary M.
/ TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
/ NUMBER OF SEQUENCES: 169
/ CORRESPONDENCE ADDRESS:
/ ADDRESSER: McAndrews, Held & Malloy, Ltd.
/ STREET: 500 West Madison Street, 34th floor
/ CITY: Chicago
/ STATE: Illinois
/ COUNTRY: USA
/ ZIP: 60661
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/488,113B
/ FILING DATE: 07-JUN-1995
/ CLASSIFICATION: 530
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/425,336
/ FILING DATE: 18-APR-1995
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/064,691
/ FILING DATE: 12-MAY-1993
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 07/988,430
/ FILING DATE: 09-DEC-1992
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 07/901,707
/ FILING DATE: 19-JUN-1992
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 07/787,567
/ FILING DATE: 04-NOV-1991
/ ATTORNEY/AGENT INFORMATION:
/ NAME: McNicholas, Janet M.
/ REGISTRATION NUMBER: 32,918
/ REFERENCE/DOCKET NUMBER: 11022US07/200-70.P3.C2A
/ TELEPHONE: 312/707-8889
/ TELEFAX: 312/707-9155
/ TELEX: 650 388-1248
/ INFORMATION FOR SEQ ID NO: 7:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 263 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ US-08-488-113B-7

Query Match 42.7%; Score 41; DB 1; Length 263;
Best Local Similarity 40.0%; Pred. No. 25;
Matches 6; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 2 IFNYKGNVLINKDI 16
Db 52 LFNYDGKTTTVAVDV 66

RESULT 15
US-08-477-484B-7
/ Sequence 7, Application US/08477484B
/ Patent No. 5756699
/ GENERAL INFORMATION:
/ APPLICANT: Better, Marc D.
/ APPLICANT: Carroll, Stephen F.
/ APPLICANT: Studnika, Gary M.
/ TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
```

```
/
/ TITLE OF INVENTION: Proteins
/ NUMBER OF SEQUENCES: 169
/ CORRESPONDENCE ADDRESS:
/ ADDRESSER: McAndrews, Held & Malloy, Ltd.
/ STREET: 500 West Madison Street, 34th floor
/ CITY: Chicago
/ STATE: Illinois
/ COUNTRY: USA
/ ZIP: 60661
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/477,484B
/ FILING DATE: 07-JUN-1995
/ CLASSIFICATION: 530
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/425,336
/ FILING DATE: 18-APR-1995
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/064,691
/ FILING DATE: 12-MAY-1993
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 07/988,430
/ FILING DATE: 09-DEC-1992
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 07/901,707
/ FILING DATE: 19-JUN-1992
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 07/787,567
/ FILING DATE: 04-NOV-1991
/ ATTORNEY/AGENT INFORMATION:
/ NAME: McNicholas, Janet M.
/ REGISTRATION NUMBER: 32,918
/ REFERENCE/DOCKET NUMBER: 11022US07/200-70.P3.C2A
/ TELEPHONE: 312/707-8889
/ TELEFAX: 312/707-9155
/ TELEX: 650 388-1248
/ INFORMATION FOR SEQ ID NO: 7:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 263 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ US-08-477-484B-7

Query Match 42.7%; Score 41; DB 1; Length 263;
Best Local Similarity 40.0%; Pred. No. 25;
Matches 6; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 2 IFNYKGNVLINKDI 16
Db 52 LFNYDGKTTTVAVDV 66

Search completed: January 9, 2002, 14:59:44
Job time: 71 sec
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; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 904-375-8100
; TELEFAX: 904-372-5800
; INFORMATION FOR SEQ ID NO: 28:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 236 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-307-499-28

Query Match 26.7%; Score 50.5; DB 1; Length 236;
Best Local Similarity 42.3%; Pred. No. 4.3;
Matches 11; Conservative 4; Mismatches 10; Indels 1; Gaps 1;

QY 1 VIFNYK-GKNVLINKDIRCKDDDETH 25
DB 164 IINTYKEGDTISINIRLCKDDIIKH 189

RESULT 5
US-09-299-268-28
; Sequence 28, Application US/09299268
; Patent No. 6217882
; GENERAL INFORMATION:
; APPLICANT: Moyer, Richard W.
; APPLICANT: Vi uela, Eladio
; APPLICANT: Gibbs, E.P.J.
; TITLE OF INVENTION: Use of Recombinant Swine Poxvirus as a
; TITLE OF INVENTION: Live Vaccine Vector
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David R. Saliwanchik
; STREET: 2421 N.W. 41st Street, Suite A-1
; CITY: Gainesville
; STATE: Florida
; COUNTRY: U.S.A.
; ZIP: 32606

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/299,268
; FILING DATE:

; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/901,127
; FILING DATE:
; APPLICATION NUMBER: US 07/908,241
; FILING DATE: 1-JUL-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/908,630
; FILING DATE: 29-JUN-1992
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/342,212
; FILING DATE: 21-APR-1992

; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Saliwanchik, David R.
; REGISTRATION NUMBER: 31,794
; REFERENCE/DOCKET NUMBER: UF35.1.FWCCI
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 904-375-8100
; TELEFAX: 904-372-5800

; INFORMATION FOR SEQ ID NO: 28:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 236 amino acids
; TYPE: amino acid
; TOPOLOGY: linear

; MOLECULE TYPE: protein
US-09-299-268-28

Query Match 26.7%; Score 50.5; DB 4; Length 236;
Best Local Similarity 42.3%; Pred. No. 4.3;
Matches 11; Conservative 4; Mismatches 10; Indels 1; Gaps 1;

QY 1 VIFNYK-GKNVLINKDIRCKDDDETH 25
DB 164 IINTYKEGDTISINIRLCKDDIIKH 189

RESULT 6
US-08-996-679-63
; Sequence 63, Application US/08996679
; Patent No. 6169071
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING
; TITLE OF INVENTION: CELL ADHESION
; NUMBER OF SEQUENCES: 63
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/996,679
; FILING DATE: 23-DEC-1997

; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Maki, David J.
; REGISTRATION NUMBER: 31,392
; REFERENCE/DOCKET NUMBER: 100086.401C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 63:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear

US-08-996-679-63
Query Match 25.4%; Score 48; DB 4; Length 17;
Best Local Similarity 43.8%; Pred. No. 0.43;
Matches 7; Conservative 7; Mismatches 2; Indels 0; Gaps 0;

QY 2 IFNYKGKNVLINKDIR 17
DB 1 IWKHKGRDVLKDKVR 16

RESULT 7
US-08-939-853A-14
; Sequence 14, Application US/08939853A
; Patent No. 6203788
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR REGULATING
; TITLE OF INVENTION: CELL ADHESION

NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/939,853A

FILING DATE: 29-SEP-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.

REGISTRATION NUMBER: 32,391
REFERENCE/DOCKET NUMBER: 100086.402
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031

INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 amino acids
TYPE: amino acid

STRANDEDNESS:
TOPOLOGY: linear

US-08-939-853A-14

Query Match 25.4%; Score: 48; DB 4; Length 17;
Best Local Similarity 43.8%; Pred. No. 0.43;
Matches 7; Conservative 7; Mismatches 2; Indels 2; Gaps 0;

QY 2 IFNYKGKVNLINKDIR 17
| : |||:| : |||
DB 1 IWKKGRDVLKDKVR 16

RESULT 8

US-09-115-395-23
Sequence 23, Application US/09115395A
Patent No. 6207639
GENERAL INFORMATION:

APPLICANT: Blaschuk, Orest W.
APPLICANT: Gour, Barbara J.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NEURITE OUTGROWTH
FILE REFERENCE: 100086.401C3
CURRENT APPLICATION NUMBER: US/09/115,395A
CURRENT FILING DATE: 1998-07-14
EARLIER APPLICATION NUMBER: 08/996,679
EARLIER FILING DATE: 1997-12-23
EARLIER APPLICATION NUMBER: 08/893,534
EARLIER FILING DATE: 1997-07-11
EARLIER APPLICATION NUMBER: 60/021,612
EARLIER FILING DATE: 1996-07-12

NUMBER OF SEQ ID NOS: 77
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 23

LENGTH: 17
TYPE: PRT
ORGANISM: Artificial Sequence

FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Solid Phase

US-09-115-395-23

Query Match 25.4%; Score: 48; DB 4; Length 17;
Best Local Similarity 43.8%; Pred. No. 0.43;

Matches 7; Conservative 7; Mismatches 2; Indels 2; Gaps 0;
QY 2 IFNYKGKVNLINKDIR 17
| : |||:| : |||
DB 1 IWKKGRDVLKDKVR 16

RESULT 9

US-09-113-977C-68
Sequence 68, Application US/09113977C
Patent No. 6277824

GENERAL INFORMATION:

APPLICANT: Doherty, Patrick
APPLICANT: Blaschuk, Orest W.

APPLICANT: Gour, Barbara J.

TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING ADHESION MOLECULE

TITLE OF INVENTION: FUNCTION

FILE REFERENCE: 100086.403

CURRENT APPLICATION NUMBER: US/09/113,977C

CURRENT FILING DATE: 1998-07-10

NUMBER OF SEQ ID NOS: 87

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 68

LENGTH: 17

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: Solid Phase

OTHER INFORMATION: Synthesis

US-09-113-977C-68

Query Match 25.4%; Score: 48; DB 4; Length 17;
Best Local Similarity 43.8%; Pred. No. 0.43;
Matches 7; Conservative 7; Mismatches 2; Indels 2; Gaps 0;

QY 2 IFNYKGKVNLINKDIR 17
| : |||:| : |||
DB 1 IWKKGRDVLKDKVR 16

RESULT 10

US-08-752-238-3
Sequence 3, Application US/08752238
Patent No. 5804418

GENERAL INFORMATION:

APPLICANT: Lambowitz Dr., Alan M
APPLICANT: Mohr Dr., Georg

APPLICANT: Saldanha Dr., Roland

APPLICANT: Matsuura Dr., Manabu

TITLE OF INVENTION: Method for Preparing Nucleotide

TITLE OF INVENTION: Integrase

NUMBER OF SEQUENCES: 12

CORRESPONDENCE ADDRESS:

ADDRESSEE: CALFEE, HALTER & GRISWOLD

STREET: 800 Superior Avenue

CITY: Cleveland

STATE: Ohio

COUNTRY: US

ZIP: 44114

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/752,238

FILING DATE:

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Golrick, Mary E.

REGISTRATION NUMBER: 34,829

REFERENCE/DOCKET NUMBER: 24671/00103

TELECOMMUNICATION INFORMATION:
TELEPHONE: (216) 622-8458
TELEFAX: (216) 241-0816
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 599 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-752-238-3

Query Match 24.9%; Score 47; DB 1; Length 599;
Best Local Similarity 53.3%; Pred. No. 45;
Matches 8; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 20 DDEFTHLYTLIVRPD 34
|: || || :|||
Db 20 DEVFTRLRYLLRPD 34

RESULT 11
US-09-085-603B-3
; Sequence 3, Application US/09085603B
; Patent No. 6001608
; GENERAL INFORMATION:
; APPLICANT: Lambowitz Dr., Alan M
; APPLICANT: Mohr Dr., Georg
; APPLICANT: Saldanha Dr., Roland
; APPLICANT: Matsuura Dr., Manabu
; APPLICANT: Yang Dr., Jiam
; APPLICANT: Zimmerly Dr., Steven
; APPLICANT: Guo Dr., Huatao
; APPLICANT: Beall Dr., Clifford J.
; TITLE OF INVENTION: Methods of Making an Rnp Particle
; TITLE OF INVENTION: Having Nucleotide Integrase Activity
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CALFEE, HALTER & GRISWOLD LLP
; STREET: 800 Superior Avenue
; CITY: Cleveland
; STATE: Ohio
; COUNTRY: US
; ZIP: 44114
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/085,603B
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Docherty, Pamela A.
; REGISTRATION NUMBER: 40,591
; REFERENCE/DOCKET NUMBER: 24671/04000
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; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 599 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-085-603B-3

Query Match 24.9%; Score 47; DB 3; Length 599;
Best Local Similarity 53.3%; Pred. No. 45;
Matches 8; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 20 DDEFTHLYTLIVRPD 34
|: || || :|||
Db 20 DEVFTRLRYLLRPD 34

RESULT 12
US-09-031-897-7
; Sequence 7, Application US/09031897
; Patent No. 6027895
; GENERAL INFORMATION:
; APPLICANT: Lambowitz, Alan
; APPLICANT: Mohr, Georg
; APPLICANT: Zimmerly, Steven
; APPLICANT: Guo, Huatao
; TITLE OF INVENTION: Methods Cleaving DNA with Nucleotide
; TITLE OF INVENTION: Integrases
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Calfee, Halter & Griswold
; STREET: 800 Superior Avenue, Suite 1400
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; COUNTRY: US
; ZIP: 44114
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/031,897
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Docherty, Pamela A.
; REGISTRATION NUMBER: 40,591
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; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 599 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-031-897-7

Query Match 24.9%; Score 47; DB 3; Length 599;
Best Local Similarity 53.3%; Pred. No. 45;
Matches 8; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 20 DDEFTHLYTLIVRPD 34
|: || || :|||
Db 20 DEVFTRLRYLLRPD 34

RESULT 13
US-09-257-770-6
; Sequence 6, Application US/09257770
; Patent No. 6306596
; GENERAL INFORMATION:
; APPLICANT: Lambowitz, Allen M.
; APPLICANT: Zimmerly, Steven
; APPLICANT: Guo, Huatao
; APPLICANT: Mohr, Georg
; APPLICANT: Beall, Clifford J.
; TITLE OF INVENTION: Methods for Cleaving Single-Stranded and
; TITLE OF INVENTION: Double-Stranded DNA Substrates with Nucleotide
; TITLE OF INVENTION: Integrase
; FILE REFERENCE: 24671/04007
; CURRENT APPLICATION NUMBER: US/09/257,770

QY 5 YKGKNVLINKDIRCKDDEFTHLYTLIVRPD 34